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Patentanmeldung Nr. Patent application No. Demande de brevet n°

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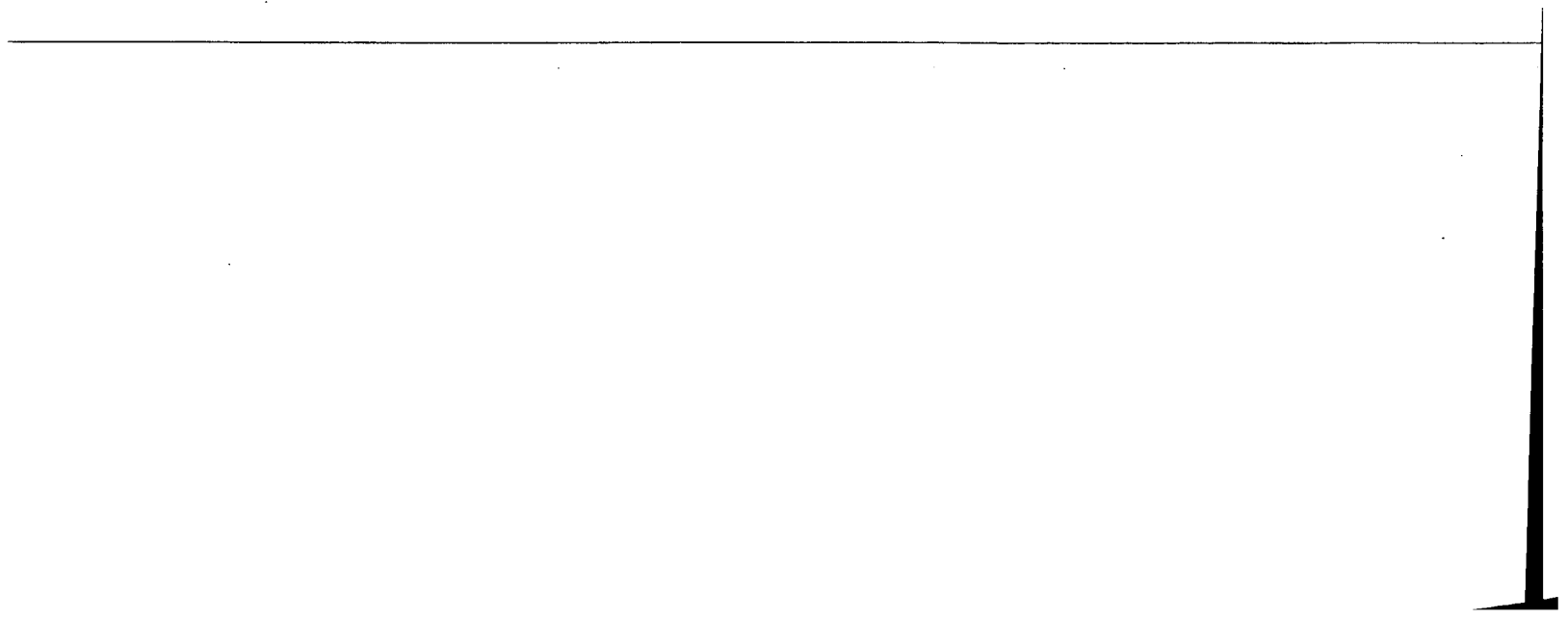
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**Novel *Neisseria meningitidis* compounds and
anti-infection applications thereof**

5

FIELD OF THE INVENTION

This invention generally relates to novel *Neisseria meningitidis* (Nm) compounds,
10 and to their anti-Nm infection applications. It more particularly relates to
polynucleotides, herein referred to as Nm polynucleotide(s), polypeptides
encoded by them (referred to herein as Nm polypeptide(s)), recombinant
materials and methods for their production. In another aspect, the invention relates
to methods for using such Nm polypeptides and Nm polynucleotides in anti-Nm
15 infection applications, such as diagnostic, prophylactic and therapeutic uses
thereof including vaccines against Nm infections. In a further aspect, the
invention relates to diagnostic assays for detecting an Nm infection.

BACKGROUND OF THE INVENTION

20 *Neisseria meningitidis* (meningococcus) is a Gram negative bacterium frequently
isolated from the human upper respiratory tract. It occasionally causes invasive
bacterial diseases such as bacteremia and meningitis. The incidence of
meningococcal disease shows geographical seasonal and annual differences
(Schwartz, B., Moore, P.S., Broome, C.V.; Clin. Microbiol. Rev. 2 (Supplement),
25 S18-S24, 1989). Most disease in temperate countries is due to strains of
serogroup B, and varies in incidence from 1-10/100,000/year total population
sometimes reaching higher values (Kaczmarek, E.B. (1997), Commun. Dis. Rep.
Rev. 7: R55-9, 1995; Scholten, R.J.P.M., Bijlmer, H.A., Poolman, J.T. *et al.* Clin.
Infect. Dis. 16: 237-246, 1993; Cruz, C., Pavez, G., Aguilar, E., *et al.* Epidemiol.

Infect. 105: 119-126, 1990).

Epidemics dominated by serogroup A meningococci, mostly in central Africa, are encountered, sometimes reaching levels up to 1000/100.000/year (Schwartz, B., Moore, P.S., Broome, C.V. Clin. Microbiol. Rev. 2 (Supplement), S18-S24, 1989). Nearly all cases as a whole of meningococcal disease are caused by serogroup A, B, C, W-135 and Y meningococci and a tetravalent A, C, W-135, Y polysaccharide vaccine is available (Armand, J., Arminjon, F., Mynard, M.C., Lafaix, C., J. Biol. Stand. 10: 335-339, 1982).

10

The polysaccharide vaccines are currently being improved by way of chemical conjugating them to carrier proteins (Lieberman, J.M., Chiu, S.S., Wong, V.K., *et al.* JAMA 275 : 1499-1503, 1996).

15 A serogroup B vaccine is not available, since the B capsular polysaccharide was found to be nonimmunogenic, most likely because it shares structural similarity to host components (Wyle, F.A., Artenstein, M.S., Brandt, M.L. *et al.* J. Infect. Dis. 126: 514-522, 1972; Finne, J.M., Leinonen, M., Mäkelä, P.M. Lancet ii.: 355-357, 1983).

20

For many years efforts have been initiated and carried out to develop meningococcal outer membrane based vaccines (de Moraes, J.C., Perkins, B., Camargo, M.C. *et al.* Lancet 340: 1074-1078, 1992; Bjune, G., Hoiby, E.A. Grommesby, J.K. *et al.* 338: 1093-1096, 1991). Such vaccines have demonstrated
25 efficacies from 57% - 85% in older children (>4 years) and adolescents, but none of them has demonstrated no significant efficacies in younger children/adults. These efficacies were further restricted to certain defined Nm strains, *i.e.* to the strain used to make the vaccine, and to related strains (*e.g.* of same electrophoretic type), without providing an efficient protection against most of the existing Nm

strains. Such vaccines does notably not provide an efficient protection against a wide range of Nm strains, such as every strain of at least one defined serogroup (such as serogroup B).

- 5 The frequency of *Neisseria meningitidis* infections has risen dramatically in the past few decades. This has been attributed to the emergence of multiply antibiotic resistant strains and an increasing population of people with weakened immune systems. It is no longer uncommon to isolate *Neisseria meningitidis* strains that are resistant to some or all of the standard antibiotics. This phenomenon has created
- 10 an unmet medical need and demand for new anti-microbial agents, vaccines, drug screening methods, and diagnostic tests for this organism.

SUMMARY OF THE INVENTION

15

The present invention relates to *Neisseria meningitidis* (Nm) polynucleotides and polypeptides, recombinant materials and methods for their production. In another aspect, the invention relates to methods for using such Nm polypeptides and polynucleotides, including prevention and treatment of Nm-related diseases.

- 20 In a further aspect, the invention relates to diagnostic assays for detecting Nm-related diseases and conditions associated with Nm infections, such as assays for detecting expression or activity of Nm polynucleotides or polypeptides.

- Various changes and modifications within the spirit and scope of the disclosed
- 25 invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

DESCRIPTION OF THE INVENTION

The invention relates to *Neisseria meningitidis* (Nm) polypeptides and polynucleotides as described in greater detail below. In particular, the invention
5 relates to Nm polynucleotides which cover the Nm genetic diversity and which correspond to Nm polypeptides of the outer membrane and/or the periplasma of Nm, and to the corresponding Nm polypeptide.

By "a polynucleotide which covers the Nm genetic diversity", it is herein meant that when assaying Nm Z2491, said polynucleotide can be observed as
10 corresponding to at least an ORF fraction of more than 250 nucleotides, advantageously more than 500 nucleotides, preferably more than 750 nucleotides, but most preferably as corresponding to a complete ORF, and that said ORF is present in more than 70%, preferably in more than 80%, and more preferably in more than 90% of the strains of a panel of Nm strains chosen according to the
15 MLST standard (multilocus sequence typing : see *e.g.* Maiden *et al.* 1998, Proc. Natl. Acad. Sci. 95 : 3140-3145) of which teaching is herein incorporated by reference. By "a polynucleotide corresponding to an ORF fraction, or a complete ORF" as above-mentioned, it is herein meant that said polynucleotide shows with said ORF fraction, or complete ORF, a sequence homology which is superior to
20 about 85%, preferably to about 90%, more preferably to about 95%, and most preferably is a 100% homologue to said ORF fraction sequence, or ORF sequence. Such a panel may comprise Nm strains chosen serogroup A Nm strains, serogroup B Nm strains, serogroup C Nm strains, serogroup W135 Nm strains, and/or serogroup Y Nm strains. An advantageous Nm panel *e.g.* comprises Nm
25 strains of the A, B, C, and W135 serogroups.

The invention relates especially to Nm compounds having the nucleotide and amino acid sequences set out in SEQ ID NO:1 to SEQ NO:90 (odd SEQ ID numbers for polynucleotides, even SEQ ID numbers for polypeptides), and are also illustrated in figures 1A to 45A (polynucleotides), and in figures 1B to 45B

(polypeptides). It is understood that sequences recited in the Sequence Listing below as "DNA" represent an exemplification of one embodiment of the invention, since those of ordinary skill will recognize that such sequences can be usefully employed in polynucleotides in general, including
5 ribopolynucleotides.

Means for assaying the presence or absence of a polynucleotide in a bacterial strain are well known techniques to the person skilled in the art, and examples of such means comprise nucleic probe hybridization (see *e.g.* dot blot experiments in the below example 1). Said polynucleotide may correspond, or be part of a gene as
10 well as, in certain Nm strains, to a pseudogene. Examples of such probes for said SEQ ID N°: 1-90 products include probes obtained by PCR amplification using the primers recited as SEQ ID N°: 97-116 and chromosomal DNA from Nm Z2491 as target DNA (see *e.g.* examples below and Table 2: SEQ ID N°97 and N°98 are nucleotidic forward and, respectively reverse primers for *dsbA*, SEQ ID
15 N°99 and N°100 are nucleotidic forward and, respectively reverse primers for *fhuA*, SEQ ID N°101 and N°102 are nucleotidic forward and, respectively reverse primers for *rni5*, SEQ ID N°103 and N°104 are nucleotidic forward and, respectively reverse primers for *tolC*, SEQ ID N°105 and N°106 are nucleotidic forward and, respectively reverse primers for *rth17*, SEQ ID N°107 and N°108 are
20 nucleotidic forward and, respectively reverse primers for *rth18*, SEQ ID N°109 and N°110 are nucleotidic forward and, respectively reverse primers for *rth19*, SEQ ID N°111 and N°112 are nucleotidic forward and, respectively reverse primers for *rth20*, SEQ ID N°113 and N°114 are nucleotidic forward and, respectively reverse primers for *rth21*, SEQ ID N°115 and N°116 are nucleotidic
25 forward and, respectively reverse primers for *fhaB*). Appropriate PCR conditions for obtaining such probes with said primers and DNA template can be determined by the person skilled in the art ; as an example, these conditions may be : 1 $\mu\text{g} \cdot \text{mL}^{-1}$ of template DNA ; reaction buffer (10 mM Tris-Cl, pH 8.0, 50 mM KCl, 1.5 mM MgCl_2 , 0.001% gelatin) ; dATP, dCTP, dGTP and dTTP (200 μM each);

dimethylsulfoxide (5%); forward and reverse primers (100 nM each) and Taq polymerase ; PCR incubation: 1 min at 94°C, 30 cycles of 1 min at 94° C, 1.5 min at 5°C below the T_m of the oligonucleotide primers, and 2 min at 72° C followed by incubation for 5 min at 72° C.

5

It is understood that sequences recited herein as corresponding to any of SEQ ID N°:1-90 represent an exemplification of one embodiment of the invention since those of ordinary skill in the art will recognize that these sequences correspond to those identified on a panel of Nm strains constituted of Nm Z2491, Nm Z3524, Nm Z3842, Nm Z4667, Nm Z4707, Nm Z5005, Nm Z6466, Nm Z7176, Nm Z4662, Nm Z6904, Nm Z4259, Nm Z4673, Nm Z4683 (see "examples" below) as Nm ORF, and that variant, but homologue, *dsbA*, *fhaB*, *fhuA*, *rni5*, *rth17*, *rth18*, *rth19*, *rth20*, *rth21*, *tolC*, sequences can be found in other Nm strains. Any appropriate technique can be implemented by the skilled person, *e.g.* sequencing the products which hybridize with said primers. Such variant sequences are thus encompassed by the present invention.

It is also understood that whereas the products of SEQ ID N°: 1-90 according to the invention are of first interest because of *inter alia* their Nm genetic diversity coverage, variant but homologue products which do not cover Nm genetic diversity on such a wide basis, can also be produced by the skilled person when desired. This means that the polypeptides and polynucleotides of the invention are candidates of first interest for construction or obtention of variant but homologue products which cover only one Nm serogroup, such as serogroup B, or which cover some but not all serogroups, such as serogroups B and A. Simple screening and/or trial and error tests can provide such variant sequences without undue burden. Such variant sequences are thus encompassed by the present invention.

Polypeptides

In one aspect of the invention there are provided polypeptides of *Neisseria meningitidis* referred to herein as Nm polypeptides as well as biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

5

The present invention further provides for:

(a) an isolated polypeptide which comprises an amino acid sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, most preferably at least 97-99% or exact identity, to that of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 ;

(b) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, over the entire length of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89 respectively;

(c) a polypeptide encoded by an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity, to the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90.

The Nm polypeptide provided in SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26 are the DsbA polypeptides from *Neisseria meningitidis* strains Z2491; Z3524, Z3842, Z4667, Z4707, Z5005, Z6466, Z7176, Z4662, Z6904, Z4259, Z4673, Z4683 respectively.

The Nm polypeptide provided in SEQ ID NO : 28 is the polypeptide (348 aminoacids) corresponding to the 3' end fraction of FhaB from *Neisseria meningitidis* strains Z2491.

10

The Nm polypeptides provided in SEQ ID NO : 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52 are the FhuA polypeptides from *Neisseria meningitidis* strains Z2491, Z3524, Z3842, Z4259, Z4662; Z4667, Z4673, Z4683, Z4707, Z5005, Z6904, Z7176 respectively.

15

The Nm polypeptides provided in SEQ ID NO : 54 is the Rni5 polypeptide from *Neisseria meningitidis* strain Z2491.

The Nm polypeptides provided in SEQ ID NO : 56, 60, 62, 64 are the Rth17, respectively Rth18, Rth19, Rth20, Rth21 polypeptides from *Neisseria meningitidis* strain Z2491.

20

The Nm polypeptides provided in SEQ ID NO : 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 are the TolC polypeptides from *Neisseria meningitidis* strain Z2491, Z3524, Z4707, Z3842, Z4259, Z4662, Z4667, Z4673, Z4683, Z5005, Z6466, Z6904, Z7176 respectively.

25

The Nm polypeptides of which ORF has some correspondance (i.e. significant hit in a computer program for sequence identity determination such as a standard

BLAST program, see also the below "definitions" section), though with no significant sequence identity/similarly, with an previously described ORF in another bacteria species have been named according to this previously known ORF. This is particularly the case of DsbA, FhaB, FhuA, Rth17 and TolC (see the

5 below "examples"). The Nm polypeptides of which ORF has no significant hit with any gene of known function have been named according to the region plus a sequential number. This is particularly the case of Rni5, Rth18, Rth19, Rth20, Rth21.

10 A source of said Nm strains is given in the below "examples".

The invention also provides an immunogenic fragment of a Nm polypeptide, that is, a contiguous portion of the Nm polypeptide which has the same or substantially the same immunogenic activity as the polypeptide comprising the amino acid

15 sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90. That is to say, the fragment (if necessary when coupled to a carrier) is capable of raising an immune response which recognises the Nm polypeptide. Such an immunogenic fragment may include, for example,

20 the Nm polypeptide lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment according to the invention comprises substantially all of the extracellular domain of a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet

25 more preferably at least 95% identity, most preferably at least 97-99% identity, to that of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90.

30 A fragment is a polypeptide having an amino acid sequence that is entirely the same as part but not all of any amino acid sequence of any polypeptide of the invention. As with Nm polypeptides, fragments may be "free-standing," or

comprised within a larger polypeptide of which they form a part or region, most preferably as a single continuous region in a single larger polypeptide.

Preferred fragments include, for example, truncation polypeptides having a portion
5 of an amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, or of variants thereof, such as a continuous series of residues that includes an amino- and/or carboxyl-terminal amino acid sequence. Degradation forms of the polypeptides of the invention
10 produced by or in a host cell, are also preferred. Further preferred are fragments characterized by structural or functional attributes such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic
15 regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.

Further preferred fragments include an isolated polypeptide comprising an amino acid sequence having at least 15, 20, 30, 40, 50 or 100 contiguous
20 amino acids from the amino acid sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, or an isolated polypeptide comprising an amino acid sequence having at least 15, 20, 30, 40, 50 or 100 contiguous amino acids truncated or deleted from the amino
25 acid sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90.

Fragments of the polypeptides of the invention may be employed for producing
30 the corresponding full-length polypeptide by peptide synthesis; therefore, these fragments may be employed as intermediates for producing the full-length

polypeptides of the invention.

Particularly preferred are variants in which several, 5-10, 1-5, 1-3, 1-2 or 1 amino acids are substituted, deleted, or added in any combination.

5

The polypeptides, or immunogenic fragments, of the invention may be in the form of the "mature" protein or may be a part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification such as multiple histidine residues, or an additional sequence for stability during recombinant production. Furthermore, addition of exogenous polypeptide or lipid tail or polynucleotide sequences to increase the immunogenic potential of the final molecule is also considered.

10

15

In one aspect, the invention relates to genetically engineered soluble fusion proteins comprising a polypeptide of the present invention, or a fragment thereof, and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE). Preferred as an immunoglobulin is the constant part of the heavy chain of human IgG, particularly IgG1, where fusion takes place at the hinge region. In a particular embodiment, the Fc part can be removed simply by incorporation of a cleavage sequence which can be cleaved with blood clotting factor Xa.

20

Furthermore, this invention relates to processes for the preparation of these fusion proteins by genetic engineering, and to the use thereof for drug screening, diagnosis and therapy. A further aspect of the invention also relates to polynucleotides encoding such fusion proteins. Examples of fusion protein technology can be found in International Patent Application Nos.

25

WO94/29458 and WO94/22914.

The proteins may be chemically conjugated, or expressed as recombinant fusion proteins allowing increased levels to be produced in an expression system as compared to non-fused protein. The fusion partner may assist in providing T helper epitopes (immunological fusion partner), preferably T helper epitopes recognised by humans, or assist in expressing the protein (expression enhancer) at higher yields than the native recombinant protein. Preferably the fusion partner will be both an immunological fusion partner and expression enhancing partner.

Fusion partners include protein D from *Haemophilus influenzae* and the non-structural protein from influenzae virus, NS1 (hemagglutinin). Another fusion partner is the protein known as LYTA. Preferably the C terminal portion of the molecule is used. Lyta is derived from *Streptococcus pneumoniae* which synthesize an N-acetyl-L-alanine amidase, amidase LYTA, (coded by the lytA gene {Gene, 43 (1986) page 265-272}) an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of E.coli C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at its amino terminus has been described {Biotechnology: 10, (1992) page 795-798}. It is possible to use the repeat portion of the Lyta molecule found in the C terminal end starting at residue 178, for example residues 188 - 305.

The present invention also includes variants of the aforementioned polypeptides, that is polypeptides that vary from the referents by conservative amino acid

substitutions, whereby a residue is substituted by another with like characteristics. Typical such substitutions are among Ala, Val, Leu and Ile; among Ser and Thr; among the acidic residues Asp and Glu; among Asn and Gln; and among the basic residues Lys and Arg; or aromatic residues Phe and Tyr.

5

Polypeptides of the present invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

10

Polynucleotides

It is an object of the invention to provide polynucleotides, herein designated Nm polynucleotides, which cover the Nm genetic diversity above and "examples" below for a definition of "Nm genetic diversity coverage"), and which correspond to outer membrane and/or periplasma Nm polypeptides. The present invention is particularly related to such Nm polynucleotides which comprises an ORF (open Reading Frame) coding for outer membrane and/or periplasma polypeptides.

15

20

In a particularly preferred embodiment of the invention the polynucleotide comprises a sequence set out in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or a variant thereof.

25

The Nm polynucleotides provided in SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 are the *dsbA* polynucleotides (complete ORF) from *Neisseria meningitidis* strain Z2491, Z3524, Z3842, Z4667, Z4707, Z5055, Z6466, Z7176, Z4662, Z6904, Z4259, Z4673, Z4683 respectively.

The Nm polynucleotide provided in SEQ ID NO : 27 is the 3' end fraction (1047 nucleotides) of the *FhaB* ORF from *Neisseria meningitidis* strain Z2491.

5 The Nm polynucleotides provided in SEQ ID NO : 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51 are the *fhuA* polynucleotides (complete ORF) from *Neisseria meningitidis* strain Z2491, Z3524, Z3842, Z4259, Z4662, Z4667, Z4673, Z4683, Z4707, Z5005, Z6904, Z7176 respectively.

10 The Nm polynucleotide provided in SEQ ID NO : 53 is the *rni5* polynucleotide (complete ORF) from *Neisseria meningitidis* strain Z2491.

The Nm polynucleotides provided in SEQ ID NO : 55, 57, 59, 61, 63 are the *rth17*, respectively *rth18*, *rth19*, *rth20*, *rth21* polynucleotides (complete ORF)
15 from *Neisseria meningitidis* strain Z2491.

The Nm polynucleotides provided in SEQ ID NO : 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89 are the *tolC* polynucleotides (complete ORF) from *Neisseria meningitidis* strain Z2491, Z3524, Z4707, Z3842, Z4259, Z4662, Z4667, Z4673,
20 Z4683, Z5005, Z6466, Z6904, Z7176 respectively.

As above explained for Nm polypeptides, Nm polynucleotides have been named according to the ORF with which some correspondance, though with no significant identity/similarity has been found in another species (*dsbA*, *fhaB*, *fhuA*,
25 *rth17* and *tolC*), or, when no correspondance with a gene of known function has been found said Nm polynucleotides have been named according to the Nm region in which they have been located, plus a sequential number (*rni5*, *rth18*, *rth19*, *rth20*, *rth21*).

As a further aspect of the invention there are provided isolated nucleic acid molecules encoding and/or expressing Nm polypeptides and polynucleotides, including, for example, unprocessed RNAs, ribozyme RNAs, mRNAs, cDNAs, genomic DNAs, B- and Z-DNAs. Further embodiments of the invention include
5 biologically, diagnostically, prophylactically, clinically or therapeutically useful polynucleotides and polypeptides, and variants thereof, and compositions comprising the same.

Another aspect of the invention relates to isolated polynucleotides, including at
10 least one full length gene, that encodes a Nm polypeptide having a deduced amino acid sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, and polynucleotides closely related thereto and variants thereof.

15

In another particularly preferred embodiment of the invention there is a Nm polypeptide from *Neisseria meningitidis* comprising or consisting of an amino acid sequence of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70,
20 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, or a variant thereof.

Using the information provided herein, such as a polynucleotide sequence set out in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81,
25 83, 85, 87, 89, a polynucleotide of the invention encoding Nm polypeptide may be obtained using standard cloning and screening methods, such as those for cloning and sequencing chromosomal DNA fragments from bacteria using *Neisseria meningitidis* cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a

polynucleotide sequence given in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, typically a library of clones of chromosomal DNA of *Neisseria meningitidis* in *E.coli* (such as a lambda DashII library) or some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Examples of such probes can be obtained by PCR amplification with the primers SEQ ID N°: 97-116 and with Nm Z2491 DNA as target DNA (see example 1 and Table 2 below).

10 Clones carrying DNA identical to that of the probe can then be distinguished using stringent hybridization conditions. By sequencing the individual clones thus identified by hybridization with sequencing primers designed from the original polypeptide or polynucleotide sequence it is then possible to extend the polynucleotide sequence in both directions to determine a full length gene

15 sequence. Conveniently, such sequencing is performed, for example, using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook *et al.*, *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989) (see in

20 particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Direct genomic DNA sequencing may also be performed to obtain a full length gene sequence. Illustrative of the invention, each polynucleotide set out in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, was discovered in a DNA

25 library derived from a *Neisseria meningitidis* panel (MLST).

Moreover, each DNA sequence set out in SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61,

63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89 corresponds to an open reading frame (ORF) encoding a protein having about the number of amino acid residues set forth in SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, respectively with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known to those skilled in the art. The DNA sequence set out in SEQ ID N°: 27 corresponds to the 1047 3' end fraction of the ORF encoding a protein having about the number of amino acid residues set forth in SEQ ID NO: 28.

10

In a further aspect, the present invention provides for an isolated polynucleotide comprising or consisting of:

(a) a polynucleotide sequence which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or exact identity to SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, over the entire length of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89;

(b) a polynucleotide sequence encoding a polypeptide which has at least 70% identity, preferably at least 80% identity, more preferably at least 90% identity, yet more preferably at least 95% identity, even more preferably at least 97-99% or 100% exact, to the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 over the entire length of SEQ ID NO : 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 respectively.

A polynucleotide encoding a polypeptide of the present invention may be obtained by a process which comprises the steps of screening an appropriate library under stringent hybridization conditions (for example, using a temperature in the range of 45 – 65°C and an SDS concentration from 0.1 – 1%) with a labeled or detectable probe consisting of or comprising the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, or a fragment thereof; and isolating a full-length gene and/or genomic clones containing said polynucleotide sequence.

The invention provides a polynucleotide sequence identical over its entire length to a coding sequence (open reading frame) in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89. Also provided by the invention is a coding sequence for a mature polypeptide or a fragment thereof, by itself as well as a coding sequence for a mature polypeptide or a fragment in reading frame with another coding sequence, such as a sequence encoding a leader or secretory sequence, a pre-, or pro- or prepro-protein sequence. The polynucleotide of the invention may also contain at least one non-coding sequence, including for example, but not limited to at least one non-coding 5' and 3' sequence, such as the transcribed but non-translated sequences, ~~termination signals (such as rho-dependent and rho-independent termination signals)~~, ribosome binding sites, Kozak sequences, sequences that stabilize mRNA, introns, and polyadenylation signals. The polynucleotide sequence may also comprise additional coding sequence encoding additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and

described in Gentz *et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA peptide tag (Wilson *et al.*, *Cell* 37: 767 (1984), both of which may be useful in purifying polypeptide sequence fused to them. Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene
5 and its naturally associated sequences that control gene expression.

The nucleotide sequence encoding Nm polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90
10 may be identical to the polypeptide encoding sequence contained in Nm nucleotides of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, respectively. Alternatively it may be a sequence, which as a result of the redundancy (degeneracy) of the genetic
15 code, also encodes the polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90.

The term "polynucleotide encoding a polypeptide" as used herein encompasses
20 polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a *Neisseria meningitidis* polypeptide having an amino acid sequence set out in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90. The term also encompasses polynucleotides that
25 include a single continuous region or discontinuous regions encoding the polypeptide (for example, polynucleotides interrupted by integrated phage, an integrated insertion sequence, an integrated vector sequence, an integrated transposon sequence, or due to RNA editing or genomic DNA reorganization) together with additional regions, that also may contain coding and/or non-coding
30 sequences.

The invention further relates to variants of the polynucleotides described herein that encode variants of a polypeptide having a deduced amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90. Fragments of polynucleotides of the invention may be used, for example, to synthesize full-length polynucleotides of the invention.

Further particularly preferred embodiments are polynucleotides encoding Nm variants, that have the amino acid sequence of Nm polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90 in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, modified, deleted and/or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, that do not alter the properties and activities of Nm polypeptide.

Further preferred embodiments of the invention are polynucleotides that are at least 70% identical over their entire length to a polynucleotide encoding Nm polypeptide having an amino acid sequence set out in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, and polynucleotides that are complementary to such polynucleotides. Alternatively, ~~most highly preferred are polynucleotides that comprise a region that is at least~~ 80% identical over its entire length to a polynucleotide encoding Nm polypeptide and polynucleotides complementary thereto. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at

least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides encoding polypeptides that retain
5 substantially the same biological function or activity as the mature polypeptide encoded by a DNA of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89.

10 In accordance with certain preferred embodiments of this invention there are provided polynucleotides that hybridize, particularly under stringent conditions, to Nm polynucleotide sequences, such as those polynucleotides in SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89.

15

The invention further relates to polynucleotides that hybridize to the polynucleotide sequences provided herein. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the polynucleotides described herein. As herein used, the terms "stringent conditions"
20 and "stringent hybridization conditions" mean hybridization occurring only if there is at least 95% and preferably at least 97% identity between the sequences. A specific example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's
25 solution, 10% dextran sulfate, and 20 micrograms/ml of denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11

therein. Solution hybridization may also be used with the polynucleotide sequences provided by the invention.

The invention also provides a polynucleotide consisting of or comprising a polynucleotide sequence obtained by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89 under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or a fragment thereof; and isolating said polynucleotide sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers fully described elsewhere herein. An appropriate library may e.g. be a lambda DashII library containing Nm Z2491 ADN fragments from about 12 to about 23 kb.

As discussed elsewhere herein regarding polynucleotide assays of the invention, for instance, the polynucleotides of the invention, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding Nm polypeptides, and to isolate cDNA and genomic clones of other genes that have a high identity, particularly high sequence identity, to the Nm gene. Such probes generally will comprise at least 15 nucleotide residues or base pairs. Preferably, such probes will have at least 30 nucleotide residues or base pairs and may have at least 50 nucleotide residues or base pairs. Particularly preferred probes will have at least 20 nucleotide residues or base pairs and will have less than 30 nucleotide residues or base pairs.

A coding region of a Nm gene may be isolated by screening using a DNA sequence provided in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.

There are several methods available and well known to those skilled in the art to obtain full-length DNAs, or extend short DNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman, *et al.*, *PNAS USA* 85: 8998-9002, 1988). Recent modifications of the technique, exemplified by the Marathon™ technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon™ technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the "missing" 5' end of the DNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using "nested" primers, that is, primers designed to anneal within the amplified product (typically an adaptor specific primer that anneals further 3' in the adaptor sequence and a gene specific primer that anneals further 5' in the selected gene sequence). The products of this reaction can then be analyzed by DNA sequencing and a full-length DNA constructed either by joining the product directly to the existing DNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the design of the 5' primer.

The polynucleotides and polypeptides of the invention may be employed, for

example, as research reagents and materials for discovery of treatments of and diagnostics for Nm-related diseases, particularly human Nm-related diseases, as further discussed herein relating to polynucleotide assays.

- 5 The polynucleotides of the invention that are oligonucleotides derived from a sequence of SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, may be used in the processes herein as described, but preferably for PCR, to determine whether or not the
- 10 polynucleotides identified herein in whole or in part are transcribed in bacteria in infected tissue. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.
- 15 The invention also provides polynucleotides that encode a polypeptide that is the mature protein plus additional amino or carboxyl-terminal amino acids, or amino acids interior to the mature polypeptide (when the mature form has more than one polypeptide chain, for instance). Such sequences may play a role in processing of a protein from precursor to a mature form, may allow protein transport, may
- 20 lengthen or shorten protein half-life or may facilitate manipulation of a protein for assay or production, among other things. As generally is the case *in vivo*, the additional amino acids may be processed away from the mature protein by cellular enzymes.
- 25 For each and every polynucleotide of the invention there is provided a polynucleotide complementary to it. It is preferred that these complementary polynucleotides are fully complementary to each polynucleotide with which they are complementary.

A precursor protein, having a mature form of the polypeptide fused to one or more prosequences may be an inactive form of the polypeptide. When prosequences are removed such inactive precursors generally are activated. Some or all of the prosequences may be removed before activation. Generally, such precursors are
5 called proproteins.

In addition to the standard A, G, C, T/U representations for nucleotides, the term "N" may also be used in describing certain polynucleotides of the invention. "N" means that any of the four DNA or RNA nucleotides may
10 appear at such a designated position in the DNA or RNA sequence, except it is preferred that N is not a nucleic acid that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

15

In sum, a polynucleotide of the invention may encode a mature protein, a mature protein plus a leader sequence (which may be referred to as a preprotein), a precursor of a mature protein having one or more prosequences that are not the leader sequences of a preprotein, or a preproprotein, which is a precursor to a
20 proprotein, having a leader sequence and one or more prosequences, which generally are removed during processing steps that produce active and mature forms of the polypeptide.

In accordance with an aspect of the invention, there is provided the use of a
25 polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of

plasmid DNA into muscles (Wolff *et al.*, *Hum Mol Genet* (1992) 1: 363, Manthorpe *et al.*, *Hum. Gene Ther.* (1983) 4: 419), delivery of DNA complexed with specific protein carriers (Wu *et al.*, *J Biol Chem.* (1989) 264: 16985), coprecipitation of DNA with calcium phosphate (Benvenisty & Reshef, *PNAS USA*, (1986) 83: 9551), encapsulation of DNA in various forms of liposomes (Kaneda *et al.*, *Science* (1989) 243: 375), particle bombardment (Tang *et al.*, *Nature* (1992) 356:152, Eisenbraun *et al.*, *DNA Cell Biol* (1993) 12: 791) and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, *PNAS USA* (1984) 81: 5849).

10

Vectors, Host Cells, Expression Systems

The invention also relates to vectors that comprise a polynucleotide or polynucleotides of the invention, host cells that are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the invention.

20

Recombinant polypeptides of the present invention may be prepared by processes well known in those skilled in the art from genetically engineered host cells comprising expression systems. Accordingly, in a further aspect, the present invention relates to expression systems that comprise a polynucleotide or polynucleotides of the present invention, to host cells which are genetically engineered with such expression systems, and to the production of polypeptides of the invention by recombinant techniques.

25

For recombinant production of the polypeptides of the invention, host cells can be

genetically engineered to incorporate expression systems or portions thereof or polynucleotides of the invention. Introduction of a polynucleotide into the host cell can be effected by methods described in many standard laboratory manuals, such as Davis, *et al.*, *BASIC METHODS IN MOLECULAR BIOLOGY*, (1986) and
5 Sambrook, *et al.*, *MOLECULAR CLONING: A LABORATORY MANUAL*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989), such as, calcium phosphate transfection, DEAE-dextran mediated transfection, transvection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction and infection.

10

Representative examples of appropriate hosts include bacterial cells, such as cells of streptococci, staphylococci, enterococci, *E. coli*, streptomyces, cyanobacteria, *Bacillus subtilis*, and *Neisseria meningitidis*; fungal cells, such as cells of a yeast, *Kluveromyces*, *Saccharomyces*, a basidiomycete, *Candida albicans* and
15 *Aspergillus*; insect cells such as cells of *Drosophila* S2 and *Spodoptera* Sf9; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, 293, CV-1 and Bowes melanoma cells; and plant cells, such as cells of a gymnosperm or angiosperm.

20

A great variety of expression systems can be used to produce the polypeptides of the invention. Such vectors include, among others, chromosomal-, episomal- and virus-derived vectors, for example, vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements,
from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses,
25 pseudorabies viruses, picornaviruses, retroviruses, and alphaviruses and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids. The expression system constructs may contain control regions that regulate as well as engender expression. Generally, any system or vector suitable to maintain, propagate or

express polynucleotides and/or to express a polypeptide in a host may be used for expression in this regard. The appropriate DNA sequence may be inserted into the expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.*, *MOLECULAR CLONING, A*
5 *LABORATORY MANUAL*, (*supra*).

In recombinant expression systems in eukaryotes, for secretion of a translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be
10 incorporated into the expressed polypeptide. These signals may be endogenous to the polypeptide or they may be heterologous signals.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or
15 ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, ion metal affinity chromatography (IMAC) is employed for purification. Well known techniques for refolding proteins may be
20 employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation and or purification.

The expression system may also be a recombinant live microorganism, such as a virus or bacterium. The gene of interest can be inserted into the genome of a
25 live recombinant virus or bacterium. Inoculation and *in vivo* infection with this live vector will lead to *in vivo* expression of the antigen and induction of immune responses. Viruses and bacteria used for this purpose are for instance: poxviruses (*e.g.* vaccinia, fowlpox, canarypox), alphaviruses (Sindbis virus, Semliki Forest Virus, Venezuelan Equine Encephalitis Virus), adenoviruses,

adeno-associated virus, picornaviruses (poliovirus, rhinovirus), herpesviruses (varicella zoster virus, *etc.*), *Listeria*, *Salmonella*, *Shigella*, BCG. These viruses and bacteria can be virulent, or attenuated in various ways in order to obtain live vaccines. Such live vaccines also form part of the invention.

5

Diagnostic, Prognostic, Serotyping and Mutation Assays

This invention is also related to the use of Nm polynucleotides and Nm polypeptides of the invention for use as diagnostic reagents. Detection of Nm polynucleotides and/or polypeptides in an eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of Nm-related disease, staging of disease or response of an infectious organism to drugs. Eukaryotes, particularly mammals, and especially humans, particularly those infected or suspected to be infected with an organism comprising the Nm gene or protein, may be detected at the nucleic acid or amino acid level by a variety of well known techniques as well as by methods provided herein.

Polypeptides and polynucleotides for prognosis, diagnosis or other analysis may be obtained from a putatively infected and/or infected individual's bodily materials. Polynucleotides from any of these sources, particularly DNA or RNA, may be used directly for detection or may be amplified enzymatically by using PCR or any other amplification technique prior to analysis. RNA, particularly mRNA, cDNA and genomic DNA may also be used in the same ways. Using amplification, characterization of the species and strain of infectious or resident organism present in an individual, may be made by an analysis of the genotype of a selected polynucleotide of the organism. Deletions and insertions can be detected by a change in size of the amplified product in comparison to a genotype of a reference sequence selected from a related organism, preferably a different species of the same genus or a different strain of the same species. Point mutations

- can be identified by hybridizing amplified DNA to labeled Nm polynucleotide sequences. Perfectly or significantly matched sequences can be distinguished from imperfectly or more significantly mismatched duplexes by DNase or RNase digestion, for DNA or RNA respectively, or by detecting differences in melting
- 5 temperatures or renaturation kinetics. Polynucleotide sequence differences may also be detected by alterations in the electrophoretic mobility of polynucleotide fragments in gels as compared to a reference sequence. This may be carried out with or without denaturing agents. Polynucleotide differences may also be detected by direct DNA or RNA sequencing. See, for example, Myers *et al.*,
- 10 *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be revealed by nuclease protection assays, such as RNase, V1 and S1 protection assay or a chemical cleavage method. See, for example, Cotton *et al.*, *Proc. Natl. Acad. Sci., USA*, 85: 4397-4401 (1985).
- 15 In another embodiment, an array of oligonucleotides probes comprising Nm nucleotide sequence or fragments thereof can be constructed to conduct efficient screening of, for example, genetic mutations, serotype, taxonomic classification or identification. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular
- 20 genetics including gene expression, genetic linkage, and genetic variability (see, for example, Chee *et al.*, *Science*, 274: 610 (1996)).

Thus in another aspect, the present invention relates to a diagnostic kit which comprises:

- 25 (a) at least one polynucleotide of the present invention, preferably the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or a fragment thereof ; and/or
- (b) at least one nucleotide sequence complementary to that of (a); and/or

(c) at least one polypeptide of the present invention, preferably the polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, or a fragment thereof; and/or

5 (d) at least one antibody to a polypeptide of the present invention, preferably to the polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90.

10 It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a Nm-related disease.

This invention also relates to the use of polynucleotides of the present invention as
15 diagnostic reagents. Detection of a mutated form of a polynucleotide of the invention, preferably, SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, which is associated with a Nm-related disease or pathogenicity will provide a diagnostic tool that can add to, or define, a
20 diagnosis of said disease, a prognosis of a course of disease, a determination of a stage of disease, or a susceptibility to said disease, which results from under-expression, over-expression or altered expression of the polynucleotide. Organisms, particularly infectious organisms, carrying mutations in such
polynucleotide may be detected at the polynucleotide level by a variety of
25 techniques, such as those described elsewhere herein.

Cells from an organism carrying mutations or polymorphisms (allelic variations) in a polynucleotide and/or polypeptide of the invention may also be detected at the polynucleotide or polypeptide level by a variety of techniques, to allow for

serotyping, for example. For example, RT-PCR can be used to detect mutations in the RNA. It is particularly preferred to use RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA, cDNA or genomic DNA may also be used for the same purpose, PCR. As an example, PCR
5 primers complementary to a polynucleotide encoding Nm polypeptide can be used to identify and analyze mutations.

The invention further provides primers with 1, 2, 3 or 4 nucleotides removed from the 5' and/or the 3' end. These primers may be used for, among other things,
10 amplifying Nm DNA and/or RNA isolated from a sample derived from an individual, such as a bodily material. The primers may be used to amplify a polynucleotide isolated from an Nm-infected individual, such that the polynucleotide may then be subject to various techniques for elucidation of the polynucleotide sequence. In this way, mutations in the polynucleotide sequence
15 may be detected and used to diagnose and/or prognose the infection or its stage or course, or to serotype and/or classify the infectious agent.

The invention further provides a process for diagnosing infections caused by *Neisseria meningitidis*, comprising determining from a sample derived from an
20 individual, such as a bodily material, an increased level of expression of polynucleotide having a sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89. Increased or decreased expression of a Nm polynucleotide can be measured using any one of
25 the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting, spectrometry and other hybridization methods.

In addition, a diagnostic assay in accordance with the invention for detecting over-

expression of Nm polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a Nm polypeptide, in a sample derived from a host, such as a bodily material, are well-known to those of skill in the art. Such assay
5 methods include radioimmunoassays, competitive-binding assays, Western Blot analysis, antibody sandwich assays, antibody detection and ELISA assays.

The polynucleotides of the invention may be used as components of polynucleotide arrays, preferably high density arrays or grids. These high
10 density arrays are particularly useful for diagnostic and prognostic purposes. For example, a set of spots each comprising a different gene, and further comprising a polynucleotide or polynucleotides of the invention, may be used for probing, such as using hybridization or nucleic acid amplification, using a probes obtained or derived from a bodily sample, to determine the presence of
15 a particular polynucleotide sequence or related sequence in an individual. Such a presence may indicate the presence of a pathogen, particularly *Neisseria meningitidis*, and may be useful in diagnosing and/or prognosing a Nm-related infection or a course of infection. A grid comprising a number of variants of the polynucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19,
20 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, are preferred. Also preferred is a comprising a number of variants of a polynucleotide sequence encoding the polypeptide sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16,
18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58,
25 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90.

Antibodies

The polypeptides and polynucleotides of the invention or variants thereof, or cells

expressing the same can be used as immunogens to produce antibodies immunospecific for such polypeptides or polynucleotides respectively.

In certain preferred embodiments of the invention there are provided antibodies
5 against Nm polypeptides or polynucleotides.

Antibodies generated against the polypeptides or polynucleotides of the invention can be obtained by administering the polypeptides and/or polynucleotides of the invention, or epitope-bearing fragments of either or both, analogues of either or
10 both, or cells expressing either or both, to an animal, preferably a nonhuman, using routine protocols. For preparation of monoclonal antibodies, any technique known in the art that provides antibodies produced by continuous cell line cultures can be used. Examples include various techniques, such as those in Köhler, G. and Milstein, C., *Nature* 256: 495-497 (1975); Kozbor *et al.*, *Immunology Today* 4: 72
15 (1983); Cole *et al.*, pg. 77-96 in *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc. (1985).

Techniques for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to polypeptides or
20 polynucleotides of this invention. Also, transgenic mice, or other organisms or animals, such as other mammals, may be used to express humanized antibodies immunospecific to the polypeptides or polynucleotides of the invention. preferably, said antibodies can bind to atleast one Nm polypeptide according to the invention in *in vivo* conditions, or in *in vitro* ones mimicking *in vivo* ones, but
25 do not recognize the patient cells.

Alternatively, phage display technology may be utilized to select antibody genes with binding activities towards a polypeptide of the invention either from repertoires of PCR amplified v-genes of lymphocytes from humans

screened for possessing anti-Nm or from naive libraries (McCafferty, *et al.*, (1990), *Nature* 348, 552-554; Marks, *et al.*, (1992) *Biotechnology* 10, 779-783). The affinity of these antibodies can also be improved by, for example, chain shuffling (Clackson *et al.*, (1991) *Nature* 352: 628).

5

The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptides or polynucleotides of the invention to purify the polypeptides or polynucleotides by, for example, affinity chromatography.

- 10 Thus, among others, antibodies against Nm-polypeptide or Nm-polynucleotide may be employed to treat infections, particularly bacterial infections.

Polypeptide variants include antigenically, epitopically or immunologically equivalent variants form a particular aspect of this invention.

15

Preferably, the antibody or variant thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized," where the complementarity determining region or regions of the hybridoma-derived antibody has been
20 transplanted into a human monoclonal antibody, for example as described in Jones *et al.* (1986), *Nature* 321, 522-525 or Tempest *et al.*, (1991) *Biotechnology* 9, 266-273.

Antagonists and Agonists - Assays and Molecules

25

Polypeptides and polynucleotides of the invention may also be used to assess the binding of small molecule substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or

functional mimetics. See, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

The screening methods may simply measure the binding of a candidate
5 compound to the polypeptide or polynucleotide, or to cells or membranes
bearing the polypeptide or polynucleotide, or a fusion protein of the
polypeptide by means of a label directly or indirectly associated with the
candidate compound. Alternatively, the screening method may involve
competition with a labeled competitor. Further, these screening methods may
10 test whether the candidate compound results in a signal generated by activation
or inhibition of the polypeptide or polynucleotide, using detection systems
appropriate to the cells comprising the polypeptide or polynucleotide.
Inhibitors of activation are generally assayed in the presence of a known
agonist and the effect on activation by the agonist by the presence of the
15 candidate compound is observed. Constitutively active polypeptide and/or
constitutively expressed polypeptides and polynucleotides may be employed in
screening methods for inverse agonists or inhibitors, in the absence of an
agonist or inhibitor, by testing whether the candidate compound results in
inhibition of activation of the polypeptide or polynucleotide, as the case may
20 be. Further, the screening methods may simply comprise the steps of mixing a
candidate compound with a solution containing a polypeptide or
polynucleotide of the present invention, to form a mixture, measuring Nm
~~polypeptide and/or polynucleotide activity in the mixture, and comparing the~~
Nm polypeptide and/or polynucleotide activity of the mixture to a standard.
25 Fusion proteins, such as those made from Fc portion and Nm polypeptide, as
hereinbefore described, can also be used for high-throughput screening assays
to identify antagonists of the polypeptide of the present invention, as well as of
phylogenetically and/or functionally related polypeptides (see D. Bennett *et al.*,
J Mol Recognition, 8:52-58 (1995); and K. Johanson *et al.*, *J Biol Chem*,

270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies that bind to and/or interact with a polypeptide of the present invention may also be used to configure
5 screening methods for detecting the effect of added compounds on the production of mRNA and/or polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents which may inhibit or
10 enhance the production of polypeptide (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

The invention also provides a method of screening compounds to identify those which enhance (agonist) or block (antagonist) the action of Nm polypeptides or
15 polynucleotides, particularly those compounds that are bacteristatic and/or bactericidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising Nm polypeptide and a labeled substrate or
20 ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be a Nm agonist or antagonist. The ability of the candidate molecule to agonize or antagonize the Nm polypeptide is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, *i.e.*, without inducing the effects
25 of Nm polypeptide are most likely to be good antagonists. Molecules that bind well and, as the case may be, increase the rate of product production from substrate, increase signal transduction, or increase chemical channel activity are agonists. Detection of the rate or level of, as the case may be, production of product from substrate, signal transduction, or chemical channel activity may be

enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric, labeled substrate converted into product, a reporter gene that is responsive to changes in Nm polynucleotide or polypeptide activity, and binding assays known in the art.

5

Another example of an assay for Nm agonists is a competitive assay that combines an Nm compound according to the invention and a potential agonist with Nm compound binding molecules, recombinant Nm binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. Said Nm compound can be labeled, such as by radioactivity or a colorimetric compound, such that the number of Nm molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

10

15 Potential antagonists include, among others, small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide and/or polypeptide of the invention and thereby inhibit or extinguish its activity or expression. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, such as a binding molecule, without inducing activities induced by a Nm compound according to the invention, thereby preventing the action or expression of Nm polypeptides and/or polynucleotides by excluding Nm polypeptides and/or polynucleotides from binding.

20

25 Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules

(see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of NMEN.

5

In a further aspect, the present invention relates to genetically engineered soluble fusion proteins comprising a polypeptide of the present invention, or a fragment thereof, and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE).

10 Preferred as an immunoglobulin is the constant part of the heavy chain of human IgG, particularly IgG1, where fusion takes place at the hinge region. In a particular embodiment, the Fc part can be removed simply by incorporation of a cleavage sequence which can be cleaved with blood clotting factor Xa. Furthermore, this invention relates to processes for the preparation of these
15 fusion proteins by genetic engineering, and to the use thereof for drug screening, diagnosis and therapy. A further aspect of the invention also relates to polynucleotides encoding such fusion proteins. Examples of fusion protein technology can be found in International Patent Application Nos. WO94/29458 and WO94/22914.

20

Each of the polynucleotide sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial
25 drugs. Additionally, the polynucleotide sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide, agonist or antagonist of the invention to interfere with the initial physical interaction between a pathogen or pathogens and a eukaryotic, preferably mammalian, host responsible for sequelae of infection. In particular, the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive and/or gram negative bacteria, to eukaryotic, preferably mammalian, extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block bacterial adhesion between eukaryotic, preferably mammalian, extracellular matrix proteins and bacterial Nm proteins that mediate tissue damage and/or; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

In accordance with yet another aspect of the invention, there are provided Nm agonists and antagonists of said Nm compounds according to the invention, preferably bacteristatic or bactericidal agonists and antagonists.

The antagonists and agonists of the invention may be employed, for instance, to prevent, inhibit and/or treat Nm-related diseases.

20

In a further aspect, the present invention relates to mimotopes of the polypeptide of the invention. A mimotope is a peptide sequence, sufficiently similar to the native peptide (sequentially or structurally), which is capable of being recognised by antibodies which recognise the native peptide; or is capable of raising antibodies which recognise the native peptide when coupled to a suitable carrier.

25

Peptide mimotopes may be designed for a particular purpose by addition, deletion or substitution of elected amino acids. Thus, the peptides may be

modified for the purposes of ease of conjugation to a protein carrier. For example, it may be desirable for some chemical conjugation methods to include a terminal cysteine. In addition it may be desirable for peptides conjugated to a protein carrier to include a hydrophobic terminus distal from the conjugated terminus of the peptide, such that the free unconjugated end of the peptide remains associated with the surface of the carrier protein. Thereby presenting the peptide in a conformation which most closely resembles that of the peptide as found in the context of the whole native molecule. For example, the peptides may be altered to have an N-terminal cysteine and a C-terminal hydrophobic amidated tail. Alternatively, the addition or substitution of a D-stereoisomer form of one or more of the amino acids may be performed to create a beneficial derivative, for example to enhance stability of the peptide.

Alternatively, peptide mimotopes may be identified using antibodies which are capable themselves of binding to the polypeptides of the present invention using techniques such as phage display technology (EP 0 552 267 B1). This technique, generates a large number of peptide sequences which mimic the structure of the native peptides and are, therefore, capable of binding to anti-native peptide antibodies, but may not necessarily themselves share significant sequence homology to the native polypeptide.

Vaccines

Another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal, preferably humans, which comprises inoculating the individual with Nm polynucleotide and/or Nm polypeptide, or a fragment or variant thereof, adequate to produce antibody and/ or T cell immune response to protect said individual from infection, particularly bacterial infection and most particularly *Neisseria*

meningitidis infection. Also provided are methods whereby such immunological response slows bacterial replication. Yet another aspect of the invention relates to a method of inducing immunological response in an individual which comprises delivering to such individual a nucleic acid vector, sequence or ribozyme to direct expression of Nm polynucleotide and/or polypeptide, or a fragment or a variant thereof, for expressing Nm polynucleotide and/or polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response, such as, to produce antibody and/or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells, to protect said individual, preferably a human, from a Nm-related disease, whether that disease is already established within the individual or not. One example of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a ribozyme, a modified nucleic acid, a DNA/RNA hybrid, a DNA-protein complex or an RNA-protein complex. The expression system may also be a recombinant live micro-organism, such as a virus or a bacterium, which can be virulent, or attenuated in various ways in order to obtain live vaccines (see "Vectors, Host Cells, Expression Systems" above).

A further aspect of the invention relates to an immunological composition that when introduced into an individual, preferably a human, capable of having induced within it an immunological response, induces an immunological response in such individual to a Nm polynucleotide and/or Nm polypeptide encoded therefrom, wherein the composition comprises a recombinant Nm polynucleotide and/or polypeptide encoded therefrom and/or comprises DNA and/or RNA which encodes and expresses an antigen of said Nm polynucleotide, polypeptide encoded therefrom, or other polypeptide of the invention. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity and/or cellular

immunity, such as cellular immunity arising from CTL or CD4+ T cells.

The immunological methods and compositions according to the invention advantageously show efficacies against at least one Nm strain belonging to one serogroup, preferably against at least two Nm strains belonging to more than
5 one Nm serogroups, preferably more than two Nm serogroups, most preferably more than three Nm serogroups *e.g.* against Nm serogroups A, B, C and W135 and/or Y.

A Nm polypeptide or a fragment thereof may be fused with co-protein or
10 chemical moiety which may or may not by itself produce antibodies, but which is capable of stabilizing the first protein and producing a fused or modified protein which will have antigenic and/or immunogenic properties, and preferably protective properties. Thus fused recombinant protein, preferably further comprises an antigenic co-protein, such as lipoprotein D
15 from *Haemophilus influenzae*, Glutathione-S-transferase (GST) or beta-galactosidase, or any other relatively large co-protein which solubilizes the protein and facilitates production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system of the organism receiving the protein. The
20 co-protein may be attached to either the amino- or carboxy-terminus of the first protein.

~~Provided by this invention are compositions, particularly vaccine compositions, and methods comprising the polypeptides and/or
25 polynucleotides of the invention and immunostimulatory DNA sequences, such as those described in Sato, Y. *et al.* Science 273: 352 (1996).~~

Also, provided by this invention are methods using the described polynucleotide or particular fragments thereof, which have been shown to

encode non-variable regions of bacterial cell surface proteins, in polynucleotide constructs used in such genetic immunization experiments in animal models of infection with *Neisseria meningitidis*. Such experiments will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. It is believed that this approach will allow for the subsequent preparation of monoclonal antibodies of particular value, derived from the requisite organ of the animal successfully resisting or clearing infection, for the development of prophylactic agents or therapeutic treatments of bacterial infection, particularly *Neisseria meningitidis* infection, in mammals, particularly humans.

The invention also includes a vaccine formulation which comprises an immunogenic recombinant polypeptide and/or polynucleotide of the invention together with a suitable carrier, such as a pharmaceutically acceptable carrier.

15 The vaccine formulation according to the invention advantageously shows efficacies against at least one Nm serogroup, advantageously more than 2 Nm serogroups, preferably more than 3 Nm serogroups (e.g. Nm serogroups A, B, C and W135 and/or Y), most preferably against any Nm strain.

Since the polypeptides and polynucleotides may be broken down in the stomach, each is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, or intradermal.

20 Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteristatic compounds and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier

immediately prior to use. Preferably, the vaccine formulation according to the invention is a anti-Nm meningitidis formulation.

5 The vaccine formulation of the invention may also include adjuvant systems for enhancing the immunogenicity of the formulation. Preferably the adjuvant system raises preferentially a TH1 type of response.

10 An immune response may be broadly distinguished into two extreme catagories, being a humoral or cell mediated immune responses (traditionally characterised by antibody and cellular effector mechanisms of protection respectively). These categories of response have been termed TH1-type responses (cell-mediated response), and TH2-type immune responses (humoral response).

15 Extreme TH1-type immune responses may be characterised by the generation of antigen specific, haplotype restricted cytotoxic T lymphocytes, and natural killer cell responses. In mice TH1-type responses are often characterised by the generation of antibodies of the IgG2a subtype, whilst in the human these correspond to IgG1 type antibodies. TH2-type immune responses are
20 characterised by the generation of a broad range of immunoglobulin isotypes including in mice IgG1, IgA, and IgM.

It can be considered that the driving force behind the development of these two types of immune responses are cytokines. High levels of TH1-type cytokines
25 tend to favour the induction of cell mediated immune responses to the given antigen, whilst high levels of TH2-type cytokines tend to favour the induction of humoral immune responses to the antigen.

The distinction of TH1 and TH2-type immune responses is not absolute. In

reality an individual will support an immune response which is described as being predominantly TH1 or predominantly TH2. However, it is often convenient to consider the families of cytokines in terms of that described in murine CD4 +ve T cell clones by Mosmann and Coffman (*Mosmann, T.R. and*
5 *Coffman, R.L. (1989) TH1 and TH2 cells: different patterns of lymphokine secretion lead to different functional properties. Annual Review of Immunology, 7, p145-173*). Traditionally, TH1-type responses are associated with the production of the INF- γ and IL-2 cytokines by T-lymphocytes. Other cytokines often directly associated with the induction of TH1-type immune
10 responses are not produced by T-cells, such as IL-12. In contrast, TH2- type responses are associated with the secretion of IL-4, IL-5, IL-6 and IL-13.

It is known that certain vaccine adjuvants are particularly suited to the stimulation of either TH1 or TH2 - type cytokine responses. Traditionally the
15 best indicators of the TH1:TH2 balance of the immune response after a vaccination or infection includes direct measurement of the production of TH1 or TH2 cytokines by T lymphocytes *in vitro* after restimulation with antigen, and/or the measurement of the IgG1:IgG2a ratio of antigen specific antibody responses.

20 Thus, a TH1-type adjuvant is one which preferentially stimulates isolated T-cell populations to produce high levels of TH1-type cytokines when re-stimulated with antigen *in vitro*, and promotes development of both CD8+ cytotoxic T lymphocytes and antigen specific immunoglobulin responses
25 associated with TH1-type isotype.

Adjuvants which are capable of preferential stimulation of the TH1 cell response are described in International Patent Application No. WO 94/00153 and WO 95/17209.

3 De-O-acylated monophosphoryl lipid A (3D-MPL) is one such adjuvant. This is known from GB 2220211 (Ribi). Chemically it is a mixture of 3 De-O-acylated monophosphoryl lipid A with 4, 5 or 6 acylated chains and is
5 manufactured by Ribi Immunochem, Montana. A preferred form of 3 De-O-acylated monophosphoryl lipid A is disclosed in European Patent 0 689 454 B1 (SmithKline Beecham Biologicals SA).

Preferably, the particles of 3D-MPL are small enough to be sterile filtered
10 through a 0.22micron membrane (European Patent number 0 689 454).
3D-MPL will be present in the range of 10mg - 100mg preferably 25-50mg per dose wherein the antigen will typically be present in a range 2-50mg per dose.

Another preferred adjuvant comprises QS21, an Hplc purified non-toxic
15 fraction derived from the bark of Quillaja Saponaria Molina. Optionally this may be admixed with 3 De-O-acylated monophosphoryl lipid A (3D-MPL), optionally together with an carrier.

The method of production of QS21 is disclosed in US patent No. 5,057,540.
20

Non-reactogenic adjuvant formulations containing QS21 have been described previously (WO 96/33739). Such formulations comprising QS21 and
cholesterol have been shown to be successful TH1 stimulating adjuvants when
formulated together with an antigen.

25 Further adjuvants which are preferential stimulators of TH1 cell response include immunomodulatory oligonucleotides, for example unmethylated CpG sequences as disclosed in WO 96/02555.

Combinations of different TH1 stimulating adjuvants, such as those mentioned hereinabove, are also contemplated as providing an adjuvant which is a preferential stimulator of TH1 cell response. For example, QS21 can be formulated together with 3D-MPL. The ratio of QS21 : 3D-MPL will typically
5 be in the order of 1 : 10 to 10 : 1; preferably 1:5 to 5 : 1 and often substantially 1 : 1. The preferred range for optimal synergy is 2.5 : 1 to 1 : 1 3D-MPL: QS21.

Preferably a carrier is also present in the vaccine composition according to the
10 invention. The carrier may be an oil in water emulsion, or an aluminium salt, such as aluminium phosphate or aluminium hydroxide.

A preferred oil-in-water emulsion comprises a metabolisable oil, such as squalene, alpha tocopherol and Tween 80. In a particularly preferred aspect
15 the antigens in the vaccine composition according to the invention are combined with QS21 and 3D-MPL in such an emulsion. Additionally the oil in water emulsion may contain span 85 and/or lecithin and/or tricaprylin.

Typically for human administration QS21 and 3D-MPL will be present in a
20 vaccine in the range of 1mg - 200mg, such as 10-100mg, preferably 10mg - 50mg per dose. Typically the oil in water will comprise from 2 to 10% squalene, from 2 to 10% alpha tocopherol and from 0.3 to 3% tween 80.
~~Preferably the ratio of squalene: alpha tocopherol is equal to or less than 1 as~~
this provides a more stable emulsion. Span 85 may also be present at a level of
25 1%. In some cases it may be advantageous that the vaccines of the present invention will further contain a stabiliser.

Non-toxic oil in water emulsions preferably contain a non-toxic oil, e.g. squalane or squalene, an emulsifier, e.g. Tween 80, in an aqueous carrier. The

aqueous carrier may be, for example, phosphate buffered saline.

A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil in water emulsion is described in WO 95/17210.

5

The present invention also provides a polyvalent vaccine composition comprising a vaccine formulation of the invention in combination with other antigens, in particular antigens useful for treating cancers, or autoimmune diseases. Such a polyvalent vaccine composition may include a TH-1 inducing adjuvant as
10 hereinbefore described.

15

While the invention has been described with reference to certain Nm polypeptides and polynucleotides, it is to be understood that this covers fragments of the naturally occurring polypeptides and polynucleotides, and
15 similar polypeptides and polynucleotides with additions, deletions or substitutions which do not substantially affect the immunogenic properties of the recombinant polypeptides or polynucleotides.

Compositions, kits and administration

20

In a further aspect of the invention there are provided compositions comprising a Nm polynucleotide and/or a Nm polypeptide for administration to a cell or to a
multicellular organism.

25

The invention also relates to compositions comprising a polynucleotide and/or a polypeptides discussed herein or their agonists or antagonists. The polypeptides and polynucleotides of the invention may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to an individual. Such

compositions comprise, for instance, a media additive or a therapeutically effective amount of a polypeptide and/or polynucleotide of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration. The invention further relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention.

10 Polypeptides, polynucleotides and other compounds of the invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

~~In a further aspect, the present invention provides for pharmaceutical compositions comprising a therapeutically effective amount of a polypeptide and/or polynucleotide, such as the soluble form of a polypeptide and/or polynucleotide of the present invention, agonist or antagonist peptide or small molecule compound, in combination with a pharmaceutically acceptable carrier or excipient. Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The invention further relates to~~

pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. Polypeptides, polynucleotides and other compounds of the present invention may be employed alone or in conjunction with other compounds, such as therapeutic
5 compounds. The present invention also provides for a therapeutic composition useful in treating animals or humans with *Neisseria meningitidis*-related disease, said composition comprising at least one antibody directed against a polypeptide according to the invention, and a suitable pharmaceutical carrier. Preferably, said antibody does not recognize the patient cells.

10

The composition will be adapted to the route of administration, for instance by a systemic or an oral route. Preferred forms of systemic administration include injection, typically by intravenous injection. Other injection routes, such as subcutaneous, intramuscular, or intraperitoneal, can be used. Alternative means for
15 systemic administration include transmucosal and transdermal administration using penetrants such as bile salts or fusidic acids or other detergents. In addition, if a polypeptide or other compounds of the present invention can be formulated in an enteric or an encapsulated formulation, oral administration may also be possible. Administration of these compounds may also be topical and/or localized,
20 in the form of salves, pastes, gels, solutions, powders and the like.

25

For administration to mammals, and particularly humans, it is expected that the daily dosage level of the active agent will be from 0.01 µg/kg to 100 µg/kg, preferably from 0.1 to 10 µg/kg, typically around 1 µg/kg. The physician in
any event will determine the actual dosage which will be most suitable for an individual and will vary with the age, weight and response of the particular individual. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this invention.

The dosage range required depends on the choice of peptide, the route of administration, the nature of the formulation, the nature of the subject's condition, and the judgment of the attending practitioner. Suitable dosages, however, are in
5 the range of 0.1-100 µg/kg of subject.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.5-5 microgram/kg of antigen, and such dose is
10 preferably administered 1-3 times and with an interval of 1-3 weeks. With the indicated dose range, no adverse toxicological effects will be observed with the compounds of the invention which would preclude their administration to suitable individuals. A preferred vaccine composition is an anti-Nm meningitidis vaccine composition.

15

Wide variations in the needed dosage, however, are to be expected in view of the variety of compounds available and the differing efficiencies of various routes of administration. For example, oral administration would be expected to require higher dosages than administration by intravenous injection. Variations in these
20 dosage levels can be adjusted using standard empirical routines for optimization, as is well understood in the art.

Sequence Databases, Sequences in a Tangible Medium, and Algorithms

25 Polynucleotide and polypeptide sequences form a valuable information resource with which to determine their 2- and 3-dimensional structures as well as to identify further sequences of similar homology. These approaches are most easily facilitated by storing the sequence in a computer readable medium and then using the stored data in a known macromolecular structure program or to search a

sequence database using well known searching tools, such as the GCG program package.

Also provided by the invention are methods for the analysis of character
5 sequences or strings, particularly genetic sequences or encoded protein
sequences. Preferred methods of sequence analysis include, for example,
methods of sequence homology analysis, such as identity and similarity
analysis, DNA, RNA and protein structure analysis, sequence assembly,
cladistic analysis, sequence motif analysis, open reading frame determination,
10 nucleic acid base calling, codon usage analysis, nucleic acid base trimming,
and sequencing chromatogram peak analysis.

A computer based method is provided for performing homology identification.
This method comprises the steps of: providing a first polynucleotide sequence
15 comprising the sequence of a polynucleotide of the invention in a computer
readable medium; and comparing said first polynucleotide sequence to at least
one second polynucleotide or polypeptide sequence to identify homology.

A computer based method is also provided for performing homology
20 identification, said method comprising the steps of: providing a first
polypeptide sequence comprising the sequence of a polypeptide of the
invention in a computer readable medium; and comparing said first
polypeptide sequence to at least one second polynucleotide or polypeptide
sequence to identify homology.

25

All publications and references, including but not limited to patents and patent
applications, cited in this specification are herein incorporated by reference in
their entirety as if each individual publication or reference were specifically
and individually indicated to be incorporated by reference herein as being fully

set forth. Any patent application to which this application claims priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

DEFINITIONS

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as the case may be, as
5 determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular*
10 *Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heine, G., Academic Press, 1987; and
15 *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Methods to determine identity are designed to give the largest match between the sequences tested. Moreover, methods to determine identity are codified in publicly available computer programs.
20 Computer program methods to determine identity between two sequences include, but are not limited to, the GAP program in the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN (Altschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990), and FASTA(Pearson and Lipman Proc. Natl. Acad. Sci. USA 85; 2444-2448
25 (1988). The BLAST family of programs is publicly available from NCBI and other sources (*BLAST Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990). The well known Smith Waterman algorithm may also be used to determine identity.

Parameters for polypeptide sequence comparison include the following:

Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)

Comparison matrix: BLOSSUM62 from Henikoff and Henikoff,
Proc. Natl. Acad. Sci. USA. 89:10915-10919 (1992)

5 Gap Penalty: 8

Gap Length Penalty: 2

A program useful with these parameters is publicly available as the "gap" program from Genetics Computer Group, Madison WI. The aforementioned parameters are the default parameters for peptide comparisons (along with no
10 penalty for end gaps).

Parameters for polynucleotide comparison include the following:

Algorithm: Needleman and Wunsch, J. Mol Biol. 48: 443-453 (1970)

Comparison matrix: matches = +10, mismatch = 0

15 Gap Penalty: 50

Gap Length Penalty: 3

Available as: The "gap" program from Genetics Computer Group, Madison WI. These are the default parameters for nucleic acid comparisons.

20 A preferred meaning for "identity" for polynucleotides and polypeptides, as the case may be, are provided in (1) and (2) below.

(1) ~~Polynucleotide embodiments further include an isolated polynucleotide~~
comprising a polynucleotide sequence having at least a 70, 80, 85, 90, 95, 97
25 or 100% identity to the reference sequence of SEQ ID NO : 1, 3, 5, 7, 9, 11,
13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53,
55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, wherein
said polynucleotide sequence may be identical to the reference sequence of
SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37,

39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or may include up to a certain integer number of nucleotide alterations as compared to the reference sequence, wherein said alterations are selected from the group consisting of at least one nucleotide
 5 deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence,
 10 and wherein said number of nucleotide alterations is determined by multiplying the total number of nucleotides in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, by the integer defining the percent identity divided by 100 and then subtracting that
 15 product from said total number of nucleotides in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89:

$$n_n \leq x_n - (x_n \bullet y),$$

20

wherein n_n is the number of nucleotide alterations, x_n is the total number of nucleotides in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, y is 0.70 for 70%, 0.80 for 80%, 0.85 for
 25 85%, 0.90 for 90%, 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and \bullet is the symbol for the multiplication operator, and wherein any non-integer product of x_n and y is rounded down to the nearest integer prior to subtracting it from x_n . Alterations of a polynucleotide sequence encoding the polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42,

44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, may create nonsense, missense or frameshift mutations in this coding sequence and thereby alter the polypeptide encoded by the polynucleotide following such alterations.

5

By way of example, a polynucleotide sequence of the present invention may be identical to the reference sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, that is it may
 10 be 100% identical, or it may include up to a certain integer number of nucleic acid alterations as compared to the reference sequence such that the percent identity is less than 100% identity. Such alterations are selected from the group consisting of at least one nucleic acid deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may
 15 occur at the 5' or 3' terminal positions of the reference polynucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleic acids in the reference sequence or in one or more contiguous groups within the reference sequence. The number of nucleic acid alterations for a given percent identity is determined by multiplying the
 20 total number of nucleic acids in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, by the integer defining the percent identity divided by 100 and then subtracting that product from said
 total number of nucleic acids in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19,
 25 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, or :

$$n_n \leq x_n - (x_n \cdot y),$$

wherein n_n is the number of nucleic acid alterations, x_n is the total number of nucleic acids in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89, y is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., \cdot is the symbol for the multiplication operator, and wherein any non-integer product of x_n and y is rounded down to the nearest integer prior to subtracting it from x_n .

(2) Polypeptide embodiments further include an isolated polypeptide comprising a polypeptide having at least a 70, 77, 80, 87, 89 or 100% identity to a polypeptide reference sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, wherein said polypeptide sequence may be identical to the reference sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, or may include up to a certain integer number of amino acid alterations as compared to the reference sequence, wherein said alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence, and wherein said number of amino acid alterations is determined by multiplying the total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, by the integer defining the percent identity divided by 100 and then

subtracting that product from said total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90 :

5

$$n_a \leq x_a - (x_a \circ y),$$

wherein n_a is the number of amino acid alterations, x_a is the total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, y is 0.70 for 70%, 0.80 for 80%, 0.85 for 85%, 0.90 for 90%, 0.95 for 95%, 0.97 for 97% or 1.00 for 100%, and \circ is the symbol for the multiplication operator, and wherein any non-integer product of x_a and y is rounded down to the nearest integer prior to subtracting it from x_a .

15

By way of example, a polypeptide sequence of the present invention may be identical to the reference sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, that is it may be 100% identical, or it may include up to a certain integer number of amino acid alterations as compared to the reference sequence such that the percent identity is less than 100% identity. Such alterations are selected from the

20

group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. The number of amino acid alterations for a given % identity is determined by

25

5 multiplying the total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, by the integer defining the percent identity divided by 100 and then subtracting that product from said total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90 :

$$n_a \leq x_a - (x_a \bullet y),$$

10

wherein n_a is the number of amino acid alterations, x_a is the total number of amino acids in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90, y is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., and \bullet is the symbol for the multiplication operator, and wherein any non-integer product of x_a and y is rounded down to the nearest integer prior to subtracting it from x_a .

20 "Individual(s)," when used herein with reference to an organism, means a multicellular eukaryote, including, but not limited to a metazoan, a mammal, an ovid, a bovid, a simian, a primate, and a human.

25 "Isolated" means altered "by the hand of man" from its natural state, i.e., if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. Moreover, a polynucleotide or polypeptide that is introduced into an organism by transformation, genetic manipulation or by any other

recombinant method is "isolated" even if it is still present in said organism, which organism may be living or non-living.

5 "Polynucleotide(s)" generally refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA including single and double-stranded regions.

10 "Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid
15 substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino
20 acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide
~~may be a naturally occurring such as an allelic variant, or it may be a variant~~
that is not known to occur naturally. Non-naturally occurring variants of
25 polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis.

"Disease(s)" means any disease caused by or related to infection by at least one *Neisseria meningitidis* strain, such as Nm meningitis.

In the below examples, reference is made to figures 1 to 50 which represent (for fig. 1 to 45: "A" letters for polynucleotidic sequences, "B" letters for polypeptidic ones) :

5 - figures 1 to 13 correspond *dsbA*/DsBA sequences obtained :

 - for allele 1 :

- from Nm strain Z2491 (Fig. 1A, 1B),
- from Nm strain Z3524 (Fig. 2A, 2B),
- from Nm strain Z3842 (Fig. 3A, 3B),
- 10 - from Nm strain Z4667 (Fig. 4A, 4B),
- from Nm strain Z4707 (Fig. 5A, 5B),
- from Nm strain Z5005 (Fig. 6A, 6B),
- from Nm strain Z6466 (Fig. 7A, 7B),
- from Nm strain Z7176 (Fig. 8A, 8B),

15 - for allele 2 :

- from Nm strain Z4662 (Fig. 9A, 9B),
- from Nm strain Z6904 (Fig. 10A, 10B),

 - for allele 3 :

- from Nm strain Z4259 (Fig. 11A, 11B),
- 20 - from Nm strain Z4673 (Fig. 12A, 12B),

 - for allele 4:

- from Nm strain Z4683 (Fig. 13A, 13B),

 - figures 14A (1047 nucleotides) et 14B (348 aminoacids) correspond to the 3' end fraction of the *fhaB*, respectively FhaB, sequences obtained from Nm strain Z2491,

25

 - figures 15 to 26 correspond to *fhuA*, FhuA sequences obtained from :

- from Nm strain Z2491 (Fig. 15A, 15B),
- from Nm strain Z3524 (Fig. 16A, 16B),
- from Nm strain Z3842 (Fig. 17A, 17B),

- from Nm strain Z4259 (Fig. 18A, 18B),
- from Nm strain Z4662 (Fig. 19A, 19B),
- from Nm strain Z4667 (Fig. 20A, 20B),
- from Nm strain Z4673 (Fig. 21A, 21B),
- 5 - from Nm strain Z4683 (Fig. 22A, 22B),
- from Nm strain Z4707 (Fig. 23A, 234B),
- from Nm strain Z5005 (Fig. 24A, 24B),
- from Nm strain Z6904 (Fig. 25A, 25B),
- from Nm strain Z7176 (Fig. 26A, 26B),
- 10 - figures 27A et 27B correspond to *rni5*, respectively Rni5, sequences obtained from Nm Z2491,
- figures 28A et 28B correspond to *rth17*, respectively Rth17, sequences obtained from Nm Z2491,
- figures 29A et 29B correspond to *rth18*, respectively Rth18, sequences
- 15 obtained from Nm Z2491,
- figures 30A et 30B correspond to *rth19*, respectively Rth19, sequences obtained from Nm Z2491,
- figures 31A et 31B correspond to *rth20*, respectively Rth20, sequences obtained from Nm Z2491,
- 20 - figures 32A et 32B correspond to *rth21*, respectively Rth21, sequences obtained from Nm Z2491,
- figures 33 to 45 correspond to *tolC*/TolC sequences obtained :
 - for allele 1 :
 - from Nm strain Z2491 (Fig. 33A, 33B),
 - 25 - from Nm strain Z3524 (Fig. 34A, 34B),
 - for allele 2 :
 - from Nm strain Z4707 (Fig. 35A, 35B),
 - for allele 3 :
 - from Nm strain Z3842 (Fig. 36A, 36B),

- from Nm strain Z4259 (Fig. 37A, 37B),
- from Nm strain Z4662 (Fig. 38A, 38B),
- from Nm strain Z4683 (Fig. 39A, 39B),
- from Nm strain Z4673 (Fig. 40A, 40B),
- 5 - from Nm strain Z4667 (Fig. 41A, 41B),
- from Nm strain Z5005 (Fig. 42A, 42B),
- from Nm strain Z6466 (Fig. 43A, 43B),
- from Nm strain Z6904 (Fig. 44A, 44B),
- from Nm strain Z7176 (Fig. 45A, 45B),
- 10 - figure 46 illustrates the production of a knockout mutation of DsbA,
- figures 47A and 47B illustrate the immunofluorescence microscopy performed on wild-type and DsbA mutant bacteria with anti-recombinant DsbA antiserum (fig. 47A: wild type Nm 8013 ; fig. 47B: DsbA mutant 8013),
- figure 48 illustrates the bactericidal activity of anti-DsbA and the
- 15 corresponding pre-immune serum
- figure 49 illustrates the bactericidal activity of anti-DsbA antiserum against meningococci expressing an isogenic mutant lacking the protein DsbA,
- figure 50 illustrates Northern blot controls of the presence of DsbA in every MLST strains.

20

EXAMPLE 1 :

The examples below are carried out using standard techniques, which are well known and routine to those of skill in the art, except where otherwise described in

25 detail. The examples are illustrative, but do not limit the invention.

Strains of Nm were tested that represent the genetic diversity of this species according to MLST (Maiden *et al.* 1998, *supra*).

Table 1

Nm strain Z number	Serological group	Clonal subgroup	ST
2491	A	IV-1	4
5005	A	I	1
3524	A	III	5
6466	A	IX	60
4662	B	groupe A4	8
3842	B	ET-5 (44/76)	32
7176	B	ET-5 (MC58)	74
4673	B	Lignée 3	41
4259	C	ET-37 (FAM18)	11
6904	W135	ET-37 (ROU)	11
4690	B	Autre	25
4683	B	Autre	30
4707	B	Autre	49
4667	B	Autre	48

Their MLST assignments were : ST1 (subgroup I, strain B40); ST2 (subgroup VI,
 5 Z6835); ST4 (subgroup IV-1, Z2491 (Sarkari *et al.*, 1994 Mol. Microbiol. 13 :
 207-217)), ST5 (subgroup III, Z3524); ST8 (A4 cluster, BZ 10); ST11 (ET-37
 complex, serogroup C: FAM18 ; serogroup W135: ROU (Pron *et al.*, 1997, J.
 Infect. Dis. 176 : 1285-1292)); ST 25 (NG G40); ST30 (NG 4/88); ST32 (ET-5

complex, 44/76); ST41 (lineage 3, BZ 198); ST48 (BZ147); ST49 (297-0); ST60q (subgroup IX, 890592) et ST74 (ET-5 complex, MC58 (Virji *et al.*, 1995, Mol. Microbiol. 18 : 741-754)).

- 5 Nm were grown on GC agar (GCB, Difco), with the addition of Kellogg's defined supplement plus ferric nitrate (Kellog *et al.*, 1963) for 12 to 20 hours at 37°C in a moist atmosphere containing 5% CO₂. Liquid media were GC-PO₄ (1.5 % Protease peptone number3 (Difco), 0.5 % NaCl, 30 mM potassium phosphate, pH 7.5) and GC-Hepes (like GC-PO₄ but potassium phosphate replaced by 30 mM
10 Hepes, pH7.5) both supplemented as for the solid medium.

- Cloning of the polynucleotides coding for outer membrane and/or periplasma polypeptides in each Nm strains

- 15 By sequencing a Nm DNA library, such as a lambda DashII library containing 12-23 kb DNA fragments of Nm Z2491, nine ORF coding for outer membrane and/or periplasma polypeptides were cloned into *E. coli* and sequenced:

- *dsbA* (allele 1) SEQ ID N°: 1 (corresponding polypeptide: SEQ ID N°: 2),
- 20 - *fhuA* SEQ ID N°: 29 (corresponding polypeptide: SEQ ID N°: 30),
- *rni5* SEQ ID N°: 53 (corresponding polypeptide: SEQ ID N°: 54),
- *rth17* SEQ ID N°: 55 (corresponding polypeptide: SEQ ID N°: 56),
- *rth18* SEQ ID N°: 57 (corresponding polypeptide: SEQ ID N°: 58),
- *rth19* SEQ ID N°: 59 (corresponding polypeptide: SEQ ID N°: 60),
- 25 - *rth20* SEQ ID N°: 61 (corresponding polypeptide: SEQ ID N°: 62),
- *rth21* SEQ ID N°: 63 (corresponding polypeptide: SEQ ID N°: 64),
- *tolC* (allele 1) SEQ ID N°: 65 (corresponding polypeptide: SEQ ID N°: 66).

A further tenth ORF was identified as *fhaB*, but only a 3' end fraction of this ORF

is herewith given: SEQ ID N° 27 (1047 nucleotides).

These sequences are illustrated by figures 1A and 1B, 14A and 14B, 27A and 27B, 28A and 28B, 29A and 29B, 30A and 30B, 31A and 31B, 32A and 32B, 33A and 33B, respectively, as above-recited (fig. number + A letter: polynucleotides ; same fig. number + B letter: corresponding polypeptides).

From these 10 new products isolated from Nm Z2491, probes were constructed so as to determine whether these 9 new ORF and the complete ORF corresponding to said new *phaB* ORF fraction are also present in the MLST Nm panel. Means for obtaining such probes include PCR amplification using the primers recited as SEQ ID N°: 97-116 and chromosomal DNA from Nm Z2491 as target DNA. Appropriate PCR conditions for obtaining such probes with said primers and DNA template can be determined by the person skilled in the art ; as an example, these conditions may be : 1 $\mu\text{g.ml}^{-1}$ of template DNA ; reaction buffer (10 mM Tris-Cl, pH 8.0, 50 mM KCl, 1.5 mM MgCl_2 , 0.001% gelatin) ; dATP, dCTP, dGTP and dTTP (200 μM each); dimethylsulfoxide (5%); forward and reverse primers (100 nM each) and Taq polymerase ; PCR incubation: 1 min at 94°C, 30 cycles of 1 min at 94° C, 1.5 min at 5°C below the T_m of the oligonucleotide primers, and 2 min at 72° C followed by incubation for 5 min at 72° C. Primer sequences are given in the below Table 2, together with the size of the PCR products thus obtained:

Table 2

ORF	forward primer	5'-3' sequence	reverse primer	5'-3' sequence	size of PCR product (kb)
<i>fhaB</i> (probe, N-term)	<i>fhaB</i> -for	AAAGCACAGCACCATGGTTGCAGTAG CCGAAAC (SEQ ID N°115)	<i>fhaB</i> -rev	AGTGTCTTTAGCCTCAATTACAGCAGCA CTGCC (SEQ ID N°116)	1.40
<i>rth17</i>	<i>rth17</i> -for	ACCGTGAGGCGGACTTGGC (SEQ ID N°107)	<i>rth17</i> -rev	TGGCCCGCATTTGTCGGGTTTAAAGCCGT CTTCG (SEQ ID N°108)	0.32
<i>rth18</i> *	<i>rth18</i> -for	ATTGCGGAGGGCGAACTGG (SEQ ID N°109)	<i>rth18</i> -rev	GCTTCGCAAAAGCCGACTTG (SEQ ID N°110)	0.40
<i>rth19</i>	<i>rth19</i> -for	GGCAACCGATTGCCATCATC (SEQ ID N°111)	<i>rth19</i> -rev	TTTCCGTTTTCAGACGGCTG (SEQ ID N°112)	0.27
<i>rth20</i>	<i>rth20</i> -for	AAGACCGTAAAAATGCAGGCG (SEQ ID N°113)	<i>rth20</i> -rev	TTTCCGACTTTGCGGGGAGTG (SEQ ID N°114)	0.29
<i>rth21</i>	<i>rth21</i> -for	GGTTGGCTGCTTCAAAACGC (SEQ ID N°115)	<i>rth21</i> -rev	ATTAAATATTTTGTCCGCTTGATC (SEQ ID N°116)	0.28

* primers for *rth18* are lying upstream of the start and downstream of the stop codon.

ORF	forward primer	5'-3' sequence	reverse primer	5'-3' sequence	size of PCR product (kb)
<i>tolC</i>	tolC-for	GCCTGACACTGACGCCCTATTGCA ACATGAAC (SEQ ID N°103)	tolC-rev	TACCGTGCTTGAGCCAGTTTCTGTTCTGC TTGG (SEQ ID N°104)	1.28
<i>dsbA</i>	dsbA-for	GCTTTGACTTCATTGACCCCTGTTGG CATTGGCC (SEQ ID N°97)	dsbA-rev	TATCCACCAACTGGTCAATCGTGGTCATA CCGG (SEQ ID N°99)	0.65
<i>fhuA</i>	fhuA-for	CCACGCTGATTATTGCTTCCTTCCC TGTGCTG (SEQ ID N°99)	fhuA-rev	ACCCGGCATAGAGTCCGAACGCCAATATT TTTG (SEQ ID N°100)	2.04
<i>rni5</i>	rni5-for	TGTTTCCCACCCAAACTTAC (SEQ ID N°101)	rni5-rev	GTTCTGGATGCAGACATAG (SEQ ID N°102)	0.36

These hybridization experiments performed under usual stringency conditions led to the conclusion that the nine new ORF and the complete ORF corresponding to the new *fhaB* fraction, which were isolated from Nm Z2491, are present in every
5 Nm strain of the MLST panel. DNA dot blot hybridization was performed according to the DIG System Users Guide (Boehringer). One microliter containing 100 ng of denatured chromosomal DNA from each strain was spotted on nylon membranes (Hybond N, Amersham) and hybridized with DIG-labeled probes obtained by PCR amplification of each ORF. The hybridizations were performed
10 using high SDS buffer (Church buffer) at 37° C, and the last washing step was with 0.5 x SSC, 0.1% SDS at 50° C in order to allow approximately 30% mismatch. Positive hybridization signals were detected by chemiluminescence.

Some of these precise sequences corresponding to those initially isolated in Nm
15 Z2491 are shown on (A letter for polynucleotides; B letter for corresponding polypeptides):

- fig. 2A and 2B (Nm Z3524 ; SEQ ID N°3 and 4, respectively), fig. 3A and 3B (Nm Z4832 ; SEQ ID N°5 and 6, respectively), fig. 4A and 4B (Nm Z4667 ; SEQ ID N°7 and 8, respectively), fig. 5A and 5B (Nm Z4707 ; SEQ ID
20 N°9 and 10, respectively), fig. 6A and 6B (Nm Z5005 ; SEQ ID N°11 and 12, respectively), fig. 7A and 7B (Nm Z6466 ; SEQ ID N°13 and 14, respectively), fig. 8A and 8B (Nm Z7176 ; SEQ ID N°15 and 16, respectively), fig. 9A and 9B (Nm Z4662 ; SEQ ID N°17 and 18, respectively), fig. 10A and 10B (Nm Z6904 ; SEQ ID N°19 and 20, respectively), fig. 11A and 11B (Nm Z4259 ; SEQ ID N°21 and 22, respectively), fig. 12A and 12B (Nm Z4673 ; SEQ ID N°23 and 24, respectively), fig. 13A and 13B (Nm Z4683 ; SEQ ID N°25 and 26, respectively),
25 for *dsbA* (respectively DsbA),

- fig. 16A and 16B (Nm Z3524 ; SEQ ID N°31 and 32, respectively), fig. 17A and 17B (Nm Z3842 ; SEQ ID N°33 and 34, respectively), fig. 18A and 18B

(Nm Z4259 ; SEQ ID N°35 and 36, respectively), fig. 19A and 19B (Nm Z4662 ; SEQ ID N°37 and 38, respectively), fig. 20A and 20B (Nm Z4667 ; SEQ ID N°39 and 40, respectively), fig. 21A and 21B (Nm Z4673 ; SEQ ID N°41 and 42, respectively), fig. 22A and 22B (Nm Z4683 ; SEQ ID N°43 and 44, respectively),
5 fig. 23A and 23B (Nm Z4707 ; SEQ ID N°45 and 46, respectively), fig. 24A and 24B (Nm Z5005 ; SEQ ID N°47 and 48, respectively), fig. 25A and 25B (Nm Z6904 ; SEQ ID N°49 and 50, respectively), fig. 26A and 26B (Nm Z7176 ; SEQ ID N°51 and 52, respectively), for *fhuA* (respectively FhuA),

- fig. 34A and 34B (Nm Z3524 ; SEQ ID N°67 and 68, respectively), fig.
10 35A and 35B (Nm Z4707 ; SEQ ID N°69 and 70, respectively), fig. 36A and 36B (Nm Z3842 ; SEQ ID N°71 and 72, respectively), fig. 37A and 37B (Nm Z4259 ; SEQ ID N°73 and 74, respectively), fig. 38A and 38B (Nm Z4662 ; SEQ ID N°75 and 76, respectively), fig. 39A and 39B (Nm Z4683 ; SEQ ID N°77 and 78, respectively), fig. 40A and 40B (Nm Z4673 ; SEQ ID N°79 and 80, respectively),
15 fig. 41A and 41B (Nm Z4667 ; SEQ ID N°81 and 82, respectively), fig. 42A and 42B (Nm Z5005 ; SEQ ID N°83 and 84, respectively), fig. 43A and 43B (Nm Z6466 ; SEQ ID N°85 and 86, respectively), fig. 44A and 44B (Nm Z6904 ; SEQ ID N°87 and 88, respectively), fig. 45A and 45B (Nm Z7176 ; SEQ ID N°89 and 90, respectively), for *tolC* (respectively TolC).

20

Below is illustrated the high identity % observed for each of these compounds when comparing different Nm strains tested.

Table 3

Identity (%) between the *fhuA* DNA sequences (5 alleles) of the different Nm strains tested.

- 5 Only intact gene sequences have been compared (no pseudogenes)

	Z4683	Z4259	Z6904	Z7176
Z2491	97,2	96,9	96,2	98,7
Z4683		96,5	96,1	98,2
Z4259			98,9	98,0
Z6904				97,0

Table 4

Identity/similarly (%) between the FhuA proteins of the different Nm strains tested.

	Z4683	Z4259	Z6904	Z7176
Z2491	98,0 / 98,1	97,6 / 97,9	97,0 / 97,4	99,6
Z4683		96,7 / 97,2	96,9 / 97,2	98,4 / 98,6
Z4259			99,1 / 99,3	98,0 / 98,3
Z6904				97,4 / 97,9

10

Table 5

Identity (%) between the *dsbA* DNA sequences (4 alleles) of the different Nm strains tested.

	Z4662	Z4259	Z4683
Z2491	99,9	97,7	98,0
Z4662		97,6	97,8
Z4259			99,7

Nm strains which are below reported as linked by an "=" sign show an identical *dsbA* sequence.

Z2491=Z3524=Z3842=Z4667=Z4707=Z5005=Z6466=Z7176

5 Z4662=Z6904

Z4259=Z4673

Z4683

Table 6

10 Identity similarly (%) between the DsbA proteins (3 types) of the different Nm strains tested.

	Z4259	Z4683
Z2491	99,8 / 98,3	98,3 / 98,7
Z4259		99,6

Nm strains which are below reported as linked by an "=" sign show an identical *dsbA* sequence.

15 Z2491=Z3524=Z3842=Z4667=Z4707=Z5005=Z6466=Z7176=Z4662=Z6904

Z4259=Z4673

Z4683

Table 7

20 Identity (%) between the *tolC* DNA sequences (4 alleles) of the different Nm strains tested.

	Z4259	Z4683	Z4707
Z2491	99,8	99,7	99,9
Z4259		99,9	99,6
Z4683			99,6

Nm strains which are below reported as linked by an "=" sign show an identical *dsbA* sequence

Z2491=Z3524

Z4259=Z6904=Z3842=Z7176=Z6466=Z5005=Z4673=Z4667=Z4662

5 Z4683

Z4707 (pseudogene with a 4 pb deletion, which causes a stop codon after 16aa)

Identity / similarly between the TolC proteins (2 types) of the different NM strains tested.

10 Nm strains which are below reported as linked by an "=" sign show an identical *dsbA* sequence

Z2491 compared to Z4259 : identity = similarly = 99,8 %

Z2491=Z3524

Z4259=Z6904=Z3842=Z7176=Z6466=Z5005=Z4673=Z4667=Z4662=Z4683

15

The 45 polynucleotides herein illustrated thus appear as covering the Nm genetic diversity, as assessed by said MLST standard test. The person skilled in the art can further verify this Nm genetic diversity coverage by standard polynucleotide detection tests (e.g. with the help of said SEQ ID N°: 97-116 primers) performed

20 in any other statistically significant Nm panel, and observe that said Nm polynucleotides are present in more than 90%, preferably more than 95%, more preferably in 100% of the Nm panel.

Each of said 45 Nm polynucleotides (ORF) were assessed for homologies to

25 known proteins using standard BLAST programs as described in the below "definitions" section.

These results are illustrated in the below table 8.

Table 8. Open reading frames common to all Nm strains tested, and their correspondence (BLAST hits) with known proteins

ORF	length (aa)	Known protein					
		function	species	length (aa)	P	%identity / %similarity	Accession #
fhaB	2015	filamentous hemagglutinin	B. pertussis	3591	1e-50	25/42	P12255
rth17	181	B precursor gene 25	phage SPP1	271	4e-04	28/39	X97918
ORFs with no significant hit (length in aa)							
rth18 (78), rth19 (155), rth20 (101), rth21 (115)							
tolC	467	outer membrane protein	E. coli	495	5e-20	23/40	P02930
fhuA	703	ferrichrome iron receptor	E. coli	747	5e-26	23/40	P06971
dsbA	231	disulfide oxidoreductase	P. syringae	214	3e-18	28/47	AF036929
rni5	230	MTH939, unknown function	Methanobacterium	188	1e-7	27/47	AE000868

The products according to the invention thus appear as novel compounds.

EXAMPLE 2 : Efficacy of the products according to the invention such as DsbA (SEQ ID N°2) from *Neisseria meningitidis* for the production of anti-meningococcal vaccines

In order to be considered as a good vaccine candidate against endemic meningococcal infections, a purified protein has to induce protective antibodies against a wide range of strains representative of the meningococcal population. Subsequently, to be considered as a vaccine candidate a protein has to be immunogenic, to be expressed on the outer membrane, and to induce protective antibodies. In this example (i) we demonstrate that DsbA is expressed in a set of NM strains representative of the meningococcal population by northern blots, (ii) we purified the protein and raised antibodies in rabbit, (iii) using this polyclonal antibody and immunofluorescence of whole bacteria we localised the protein on the outer membrane, (iv) we engineered a non polar mutation and using this mutant we demonstrate that the anti DsbA polyclonal antibody has a bactericidal activity against the wild type strain and not against the isogenic mutant. In this example, DsbA (SEQ ID N°2) was purified as a recombinant protein lacking the signal sequence associated with a hexahistidine tract only in order to facilitate purification. The same procedure can be implemented by the skilled person with any preparation of DsbA isolated directly from *Neisseria meningitidis*, by immunological or biochemical means and all other recombinant forms of the protein, or similarly with any product according to the invention.

I. Northern Blot

Controls of the presence of said recombinant DsbA in every MLST Nm strain have been performed by Northern blot analysis, as below detailed. These controls have confirmed said DsbA covers Nm genetic diversity, as *e.g.* illustrated by figure 50 (Northern blots

lanes are given in the below table 9). The marker used was the RNA molecular weight marker I, digoxigenin-labeled, from Boehringer, with 9 fragments, the sizes are indicated in the blot.

5 Bacteria

Table 9:

lane	strain
1	Nm, serogroup A, subgroup IV-1
2	Nm, serogroup A, subgroup III
3	Nm, serogroup A, subgroup I
4	Nm, serogroup A, subgroup VI
5	Nm, serogroup A, subgroup IX
6	Nm, serogroup C, ET-37 complex, FAM18
7	Nm, serogroup W135, ET-37 complex, ROU
8	Nm, serogroup B, ET-5 complex, 44/76
9	Nm, serogroup B, ET-5 complex, MC58
10	Nm, serogroup B, Lineage 3
11	Nm, serogroup B, A4 cluster
12	Nm, serogroup B, ST25
13	Nm, serogroup B, ST30
14	Nm, serogroup B, ST48
15	Nm, serogroup B, ST49
16	Ng, FA1090

The *Neisseria meningitidis* strains chosen for RNA analysis represent the genetic diversity of this species according to multilocus sequence typing (MLST) (Maiden *et al.*, 1998).

10

Isolation of total RNA from *Neisseria*

Bacteria were grown on supplemented GC plates overnight at 37°C, 5% CO₂, 95% humidity. Single colonies were inoculated in 5 ml supplemented GC medium and grown at 37°C, 180 rpm until an optical density of Klett 50 was reached. 4 ml bacterial culture was pelleted by centrifugation (5000 rpm, 10 min).

RNA isolation was performed using the RNAqueous Kit (Ambion, Austin, TX, USA) according to the manufacturer's protocol: The bacterial pellet was resuspended in 350 µl Lysis/Binding Solution. 400 µl 64% ethanol were added and mixed by repeated pipetting. 400 µl of the lysate/ethanol mixture were applied to a filter cartridge and centrifuged in a microcentrifuge for 1 min. The flow-through was discarded and the remaining lysate/ethanol mixture was centrifuged through the filter. The filter cartridge was once washed with 700 µl Wash Solution #1 and twice with 500 µl Wash Solution #2/3. The wash solutions were passed through the filter by centrifugation for 1 min; the last traces of wash solution were removed by 2 min centrifugation after the last washing step. The filter cartridge was transferred to a fresh collection tube and 60 µl of elution solution was added to the center of the filter. The cartridge was incubated in a heat block at 65°C for 10 min and the eluate was recovered by centrifugation for 1 min. This elution step was repeated with another 60 µl of elution solution. The concentration of the RNA was measured in a 1:10 dilution in elution solution. The average RNA yield was around 1.5 µg/µl. RNA was stored at -80°C.

RNA electrophoresis and transfer (Northern blot)

A 1% denaturing agarose gel was prepared by dissolving 0.5 g agarose in 40.5 ml H₂O and cooling to 60°C. 5 ml 10 x MOPS buffer (0.2 M MOPS, pH 7.0, 0.05 M sodium-acetate, 0.01 M EDTA) and 4.5 ml formaldehyde (37%) were added and the gel was poured (gel size: 13 cm x 7.5 cm). 1 x MOPS was used as running buffer.

The RNA samples (ca. 3 µg per lane) were mixed with 4 volumes of gel loading solution (supplied with the RNAqueous Kit) containing 10 µg/ml ethidium bromide. The samples were heated at 65°C for 10 min and immediately put on ice. The RNA was loaded and

electrophoresis was performed at 5 V/cm until the bromophenol blue band had migrated two thirds of the length of the gel. The gel was photographed and washed for 10 min in H₂O to remove formaldehyde.

5 The RNA was transferred from the gel to Hybond N+ membrane (Amersham) by capillary transfer (Sambrook *et al.*, 1989) overnight using 20 x SSC (3 M NaCl, 0.3 M sodium citrate, pH 7.0) as transfer buffer.

The membrane was shortly washed with 2 x SSC and baked between Whatman 3MM filter paper for 30 min at 120°C.

10 Hybridization and detection

The RNA was detected using the DIG system (Boehringer Mannheim).

Labeling of the DNA probe:

Primers specific for the *dsbA* homolog of strain Z2491

15 (forward primer: 5'-GCTTTGACTTCATTGACCCTGTTGGCATTGGCC; (SEQ ID N°97)

reverse primer: 5'-TATCCACCAACTGGTCAATCGTGGTCATACCGG) SEQ ID N°98 were used in PCR amplification with DIG-labeled dUTP. Template chromosomal DNA of strain Z2491 was isolated as described (Sarkari *et al.*, 1994). The PCR reaction mixture contained template DNA (1 µg/ml); reaction buffer (10 mM Tris-Cl, pH 8.0, 50 mM KCl, 1.5 mM MgCl₂, 0.01% gelatin); PCR DIG probe synthesis mix (200 µM dATP, dCTP, 20 dGTP each, 190 µM dTTP, 10 µM digoxigenin-11-dUTP; Boehringer); forward and reverse primer (100 nM each) and Taq polymerase. The PCR reaction was incubated 1 min at 94°C, followed by 30 cycles of 1 min at 94°C, 1.5 min at 60°C and 2 min at 72°C followed by incubation for 5 min at 72°C. The labeled PCR product was purified using

25 the Qiaquick PCR Purification Kit (Qiagen).

Hybridization conditions:

For prehybridization, the membrane was incubated for 2 h at 42°C with 20 ml of hybridization solution (High SDS Buffer: 7% SDS, 50% formamide, 5 x SSC, 2% Blocking Reagent (Boehringer), 50 mM sodium-phosphate, pH 7.0, 0.1% N-

lauroylsarcosine) in a hybridization tube. This solution was replaced by 10 ml hybridization solution containing 250 ng of labeled probe. For denaturation, this solution was heated at 68°C for 10 min before adding. Hybridization was performed overnight at 42°C. After that, the membrane was washed 2 x 5 min at room temperature with 2 x SSC, 0.1 % SDS and 2 x 30 min at 68°C with 0.5 x SSC, 0.1% SDS.

Detection by chemiluminescence:

After hybridization and washing, the membrane was equilibrated for 1 min in maleic acid buffer (100 mM maleic acid, 150 mM NaCl, pH 7.5). The membrane was blocked by gentle agitation in blocking solution (1% Blocking Reagent (Boehringer) in maleic acid buffer), followed by incubation with antibody solution (Anti-Digoxigenin, Fab fragments conjugated to alkaline phosphatase, 1:10000 in blocking solution) for further 30 min. The membrane was washed 2 x 15 min with maleic acid buffer and then equilibrated for 2 min in detection buffer (100 mM Tris-Cl, 100 mM NaCl, pH 9.5). The chemiluminescence substrate CSPD was diluted 1:100 in detection buffer. The membrane was treated with CSPD-solution for 5 min at room temperature in a sealed bag. After removing the CSPD-solution, the membrane was sealed again and incubated for 15 min at 37°C. The membrane was exposed to X-ray film for 1 h.

II. Creation of an isogenic DsbA mutant of meningococci

20

Oligonucleotides were designed to amplify DNA fragments extending about 1 kilobase on either side of the first cysteine codon in *dsbA* (SEQ ID N°1) (This cysteine is immediately after the predicted site of proteolytic cleavage in the maturation of the protein DsbA). Oligonucleotides were designed such that a ligation of the two fragments recreates the

DNA sequence of DsbA and some flanking sequence, with the exception that there is an *EcoRI* restriction endonuclease site (an *EcoRI* site) in place of the DNA sequence coding for the predicted protease recognition site, the first cysteine codon is no longer present, there is an in-frame translational stop codon and the translational frame of the rest (3') of the gene is shifted by one base.

Oligonucleotides used to amplify the 5' end of the DsbA gene plus upstream sequence were:

b31331: GAACATGGATCCCGTCCACACACTTTACG
(SEQ ID N°91)

5 b31311: GCGGCCGAATTCCAACAGGGTCAATGAAGT
(SEQ ID N°92)

Oligonucleotides used to amplify the 3' end of DsbA plus downstream sequence were

b31312: CTGTTGGAATTCGGCCGCTTGTAGCAAACAGGCT
(SEQ ID N°93)

10

b31313: TAGTACGGTACCGATTCACTTGGTGCTT
(SEQ ID N°94)

In order to mutate the *dsbA* gene PCR amplification was performed using chromosomal DNA from strain 8013 (a serogroup C clinical isolate) as template.

15 Oligonucleotides b31311 and b31312 contain complementary sequences, such that mixture of the two PCR products in the presence of the two 'external' oligonucleotides b31331 and b31313 results in 'PCR ligation' forming the DNA fragment extending from the position of b31331 to that of b31313, and including the modifications described above. This fragment was cleaved with the enzymes *Bam*HI and *Kpn*I and cloned into
20 appropriately cleaved vector pBluescript II SK(+), which was then propagated in *E. coli* DH5 α . This construction was linearised by digestion with *Eco*RI. Into the *Eco*RI site was inserted a resistance cassette containing a gene encoding resistance to erythromycin and two neisserial uptake sequences (GCCGTCTGAA) which have been shown to be necessary for efficient transformation of Nm [Goodman, S. D., and Scocca, J. J. (1988).

25 Identification and arrangement of the DNA sequence recognized in specific transformation of *Neisseria gonorrhoeae*. *Proc. Natl. Acad. Sci. USA* 85, 6982-6986]. The plasmid containing the *dsbA* gene interrupted by the erythromycin resistance cassette was used to transform Nm to erythromycin resistance, selecting on 2 μ g/ml erythromycin. Chromosomal DNA, prepared from a selected transformant strain was used to back

transform the parental strain 8013 (serogroup C ; see Nassif X., D. Quai, and M. So. Transposition of Tn1545-*3 in the pathogenic Neisseriae: a genetic tool for mutagenesis, Journal of Bacteriology, 1991, 173, 2147-2154) and several hundred transformant colonies were taken to give a statistically homogeneous genetic background.

5 The transformant strain was tested by western blot in order to show that it no longer expressed the protein DsbA, using either rabbit anti-whole cell (strain Z5463) or anti-DsbA antiserum.

The overall strategy is illustrated by figure 46 which shows the production of a knockout mutation of DsbA. On this figure, ORF are shown as arrows (note that the sequence shown is that of Z2491 and that strain 8013 does not contain the ORF *rei1* ; the PCR product b31331-31311 is correspondingly shorter). The position of the oligonucleotide primers are shown as small arrows. PCR products are shown as shaded boxes. The two PCR products were ligated (fig. 46a) and cloned into the vector pBluescript. After linearisation of the plasmid by cleavage with *EcoRI*, the resistance cassette (dark grey) was inserted (fig. 46b). This construction was used to transform Nm to erythromycin resistance (fig. 46c), thus replacing the wild-type *dsbA* gene with that interrupted with the resistance cassette.

III. Cloning and expression of DsbA for use in production of anti-DsbA antiserum

20 Overview of cloning strategy. The antigen DsbA is predicted to be a lipoprotein, whose lipophilic signal sequence is cleaved to leave an N-terminal cysteine residue which is subsequently modified by the addition of (a) fatty acid molecule(s) for anchorage in the outer membrane [Pugsley, A. P. (1993). The complete general secretory pathway in Gram-negative bacteria. *Microbiol. Rev.* 57, 50-108]. This signal sequence is not present in the mature protein. After cloning and overexpression of the gene, if the protein were exported in large quantities to the outer membrane of the host *E. coli* it could prove toxic for the bacteria. On the basis of these considerations, the gene was not cloned in its entirety, but only the sequence coding for the predicted mature protein was cloned and

expressed. In order to minimise the metabolic load on the host bacteria, the (codon for the) N-terminal cysteine of the mature protein was replaced by a (codon for a) serine.

Primers were designed in order to amplify DNA corresponding to the predicted mature protein DsbA and to allow subsequent ligation into an expression vector which links the protein at its C-terminal end to a hexahistidine tract (His-tag) in order to facilitate subsequent purification, using a nickel affinity column.

Oligonucleotides

b31316b (GCTTGTGGTACCATATGAGCAAACAGGCTGAAACCAGT ;
SEQ ID N°95)

and b31317 (TCAATCCTCGAGTTGCGGCTTTTTCTGCTCTT ;
SEQ ID N°96) were designed to amplify a fragment from the chromosome of Nm strain Z2491. Oligonucleotide b31316b contains a recognition site for the restriction endonuclease *NdeI* (CATATG) allowing the fragment to be cloned into the expression vector pET20b(+) (Novagen R&D systems). The latter half of this site specifies the amino acid methionine, which is the N-terminal amino acid of the expressed protein. This is followed by a codon specifying serine (which was chosen to replace the N-terminal cysteine of the mature protein) and subsequently by bases corresponding to the gene sequence. The oligonucleotide b31317 causes the replacement of the gene's natural stop codon with the first three bases of an *XhoI* site (CTCGAG), which allows an in frame link to the expression vector's hexahistidine encoding sequence. Translation is terminated after the hexahistidine by a stop codon in the vector.

Overview of strategy for overexpression of the cloned protein. The expression vector takes advantage of an *NdeI* site to allow insertion of a coding DNA sequence such that the second half of this site (ATG) is recognised by the ribosome as the first amino acid of the recombinant protein to be expressed. Since cleavage by the enzyme *NdeI* is particularly inefficient near the extremity of a PCR product, it is easier to clone the PCR product using another method (either using a site incorporated into the oligonucleotide 5' to the *NdeI* site, by 'TA cloning', or by enzymatically blunting the fragment and ligating into a

'blunt-ended' restriction enzyme site) then excise the coding fragment using the enzymes *NdeI* and that at the 3' end of the gene). This fragment is then ligated into the expression vector and the resulting plasmid grown in *E. coli* strain DH5 α , which is highly transformable and will not be harmed by the expression of the potentially toxic foreign protein since it is incapable of initiating transcription from the T7 RNA polymerase promoter in the expression vectors. Plasmid isolated from DH5 α is then used to transform (at high efficiency) *E. coli* strain BL21(DE3). This strain contains a gene for T7 RNA polymerase preceded by the *lac* promoter and hence inducible by isopropyl b-D-thiogalactoside (IPTG). Addition of IPTG to the culture medium induces the transcription of the T7 RNA polymerase gene. The recombinant protein gene is read by the T7 RNA polymerase, and the transcript translated to overproduce the recombinant protein.

Cloning of the DsbA gene. The PCR products from b31316b and b31317 using chromosomal DNA as template were blunted (using the Klenow fragment of *E. coli* DNA polymerase and T4 phage polynucleotide kinase in the presence of the four deoxynucleotide triphosphates and ATP) and ligated into the *SmaI* site of plasmid pUC18. The ligation mixtures were used to transform *E. coli* DH5 α , and the resulting plasmid were cleaved with *NdeI* and *XhoI*. The liberated fragment was gel purified and ligated into the expression vector pET-20b(+). The ligation mixture was used to transform *E. coli* DH5 α , then plasmid was isolated and used to transform BL21(DE3). Individual colony isolates were screened for production of the recombinant protein by SDS-PAGE. One isolate was chosen for subsequent use in protein purification. This isolate was designated 2g:

Name	<i>E. coli</i> strain	construction	expressed protein
25	2g	BL21(DE3) pET20b(+):PCR product b31316b-b31317	DsbA-(C-terminal his tag)

Purification of the recombinant proteins. Recombinant DsbA protein was purified using an affinity column produced with Poly-His protein purification resin. Bacteria (20 to 50 isolated colonies of overnight growth on LB agar containing 100 mg/ml of ampicillin)

were inoculated into 500 ml of LB medium containing 100 mg/ml of ampicillin and incubated at 37°C in a conical flask with orbital shaking to maintain aeration. When the OD at 600 nm of the culture had reached between 0.4 and 0.5, the expression of the protein was induced by addition of IPTG to 2 mM. Growth was continued for a further 2 hours, then the bacteria were harvested by centrifugation at 3500 x g for 25 minutes. The pellets were sonicated (three times 5 minutes, on ice) in 10 ml of PBS to break the cells. The suspension was centrifuged at 15000 x g and the supernatant taken. For purification, 5 ml of the supernatant was passed through a column made from 1 ml of 'poly-His protein purification resin' (Boehringer Mannheim). The column was washed with 5 ml of PBS containing 10 mM imidazole, then 5 ml of PBS/20 mM imidazole. The recombinant DsbA protein was eluted in PBS/50 mM imidazole, then PBS/500 mM imidazole. Fractions containing pure recombinant DsbA (by SDS-PAGE analysis) were pooled and dialysed against PBS. Stocks containing recombinant DsbA at 100 µg/ml were stored at -80°C.

IV. Immunisation of a rabbit with recombinant DsbA.

New Zealand white rabbits were immunised three times at intervals of 15 days with 100 µg of recombinant DsbA (preparation 2g).

1st immunisation 2 ml of antigen '2g' in PBS:Freund's complete adjuvant (1:1)

2nd immunisation 2 ml of antigen '2g' in PBS:Freund's incomplete adjuvant (1:1)

3rd immunisation 2 ml of antigen '2g' in PBS:Freund's incomplete adjuvant (1:1)

Blood was taken from the rabbits 3 weeks after the third immunisation and allowed to clot overnight. Serum was separated from the clot by centrifugation and stored in aliquots at -80°C.

V. Immunofluorescence staining of meningococci

Meningococci were grown for 18 hours on GCB-agar (Difco), then resuspended in PBS.

- 5 Drops of suspension were immediately placed on glass microscope slides and allowed to dry at 45°C. The bacteria were fixed to the slide by adding methanol and allowing to evaporate (twice). The bacteria were pretreated with PBS containing 1% gelatin, then reacted with the primary antibody (1/1000 dilution of the rabbit anti-recombinant DsbA in PBS/gelatin) for 30 minutes at room temperature. The slides were washed twice for 2
- 10 minutes in an excess of PBS, then reacted with 1/200 dilutions the secondary antibody in PBS/gelatin (sheep anti-rabbit immunoglobulin G-Cy3-conjugate) for 30 minutes at room temperature. Slides were washed three times for 5 minutes in an excess of PBS, then the bacteria were counterstained with DAPI (1 µg/ml in PBS/10% methanol) and rinsed twice in PBS. The slides were allowed nearly to dry, then the mounting fluid 'morviol' (Sigma)
- 15 was added to the bacteria and cover slips were fixed in place. The bacteria and fixed antibodies were visualised by ultraviolet and light microscopy.

- Anti-DsbA antiserum gave a halo of reacting antibodies around the wild type Nm (8013) which was reduced to the background level of reactivity of the secondary (sheep anti-rabbit immunoglobulin G) antibody alone in the case of the DsbA mutant. These results
- 20 are illustrated by figures 47A and 47B, which show an immunofluorescence microscopy of wild-type and DsbA mutant bacteria with anti-recombinant DsbA antiserum: figure 47A, wild-type Nm 8013 reacted with anti-DsbA antiserum and revealed with anti-rabbit immunoglobulin G-Cy3 conjugate ; figure 47B, DsbA mutant 8013 reacted with anti-DsbA antiserum and revealed with anti-rabbit immunoglobulin G-Cy3 conjugate.

- 25 This demonstrates that the DsbA protein is exposed at the surface of the bacteria.

V. Assay for the bactericidal activity of the rabbit anti-recombinant DsbA antiserum

Volumes of 10 µl of PBS containing 2000 bacteria were mixed with 500 µl of freshly-

thawed rabbit serum. Volumes of 95 μ l were taken from the assays for enumeration immediately and at time points up to 90 minutes after addition of the serum. Enumeration was performed by plating 50 μ l aliquots of 10-fold dilutions of the assays onto GCB agar (Difco).

- 5 The results show that while the antiserum killed 65% of the parental meningococcus (strain 8013) within 20 minutes and all of the bacteria within 60 minutes, the preimmune serum (serum taken from the rabbit before the first immunisation) killed none after 20 minutes and only half after 60 minutes. Hence the antiserum is capable of killing heterologous meningococci (The DsbA sequence was taken from strain Z2491). This is
10 illustrated by figure 48 which shows the bactericidal activity of anti-DsbA and the corresponding preimmune antiserum.

- The bactericidal activity of the antiserum against the parental strain 8013 was compared with that against the isogenic mutant containing an interrupted DsbA gene (and shown by western blot not to express this protein). In this case freshly-thawed anti-recombinant
15 DsbA antiserum was added to the parental and to the DsbA mutant. The results show that the bactericidal activity is specific for the DsbA-expressing strain, since the parental strain was killed to a much greater extent than was the mutant. This is illustrated by figure 49, which shows the bactericidal activity of anti-DsbA antiserum against meningococci expressing an isogenic mutant lacking the protein DsbA.

SEQUENCE LISTING BRIEF SUMMARY

SEQ ID N°	Sequence nature	Nm strain source	product name	
				DsbA Allele 1
1	nucleotides	Z2491	<i>dsbA</i>	
2	aminoacids	Z2491	DsbA	
3	nucleotides	Z3524	<i>dsbA</i>	
4	aminoacids	Z3524	DsbA	
5	nucleotides	Z3842	<i>dsbA</i>	
6	aminoacids	Z3842	DsbA	
7	nucleotides	Z4667	<i>dsbA</i>	
8	aminoacids	Z4667	DsbA	
9	nucleotides	Z4707	<i>dsbA</i>	
10	aminoacids	Z4707	DsbA	
11	nucleotides	Z5005	<i>dsbA</i>	

12	aminoacids	Z5005	DsbA	
13	nucleotides	Z6466	<i>dsbA</i>	
14	aminoacids	Z6466	DsbA	
15	nucleotides	Z7176	<i>dsbA</i>	
16	aminoacids	Z7176	DsbA	
				DsbA Allele 2
17	nucleotides	Z4662	<i>dsbA</i>	
18	aminoacids	Z4662	DsbA	
19	nucleotides	Z6904	<i>dsbA</i>	
20	aminoacids	Z6904	Dsba	
				DsbA Allele 3
21	nucleotides	Z4259	<i>dsbA</i>	
22	aminoacids	Z4259	DsbA	
23	nucleotides	Z4673	<i>dsbA</i>	
24	aminoacids	Z4673	DsbA	

DsbA				Allele 4
25	nucleotides	Z4683	<i>dsbA</i>	
26	aminoacids	Z4683	DsbA	
FhaB				
27	nucleotides (3' end 1047 ones)	Z2491	<i>fhaB</i>	
28	aminoacids	Z2491	FhaB	
FhuA				
29	nucleotides	Z2491	<i>fhuA</i>	
30	aminoacids	Z2491	FhuA	
31	nucleotides	Z3524	<i>fhuA</i>	
32	aminoacids	Z3524	FhuA	
33	nucleotides	Z3842	<i>fhuA</i>	
34	aminoacids	Z3842	FhuA	
35	nucleotides	Z4259	<i>fhuA</i>	
36	aminoacids	Z4259	FhuA	
37	nucleotides	Z4662	<i>fhuA</i>	

38	aminoacids	Z4662	FhuA
39	nucleotides	Z4667	<i>fhuA</i>
40	aminoacids	Z4667	FhuA
41	nucleotides	Z4673	<i>fhuA</i>
42	aminoacids	Z4673	FhuA
43	nucleotides	Z4683	<i>fhuA</i>
44	aminoacids	Z4683	FhuA
45	nucleotides	Z4707	<i>fhuA</i>
46	aminoacids	Z4707	FhuA
47	nucleotides	Z5005	<i>fhuA</i>
48	aminoacids	Z5005	FhuA
49	nucleotides	Z6904	<i>fhuA</i>
50	aminoacids	Z6904	FhuA
51	nucleotides	Z7176	<i>fhuA</i>
52	aminoacids	Z7176	FhuA

				Rni
53	nucleotides	Z2491	<i>rni5</i>	
54	aminoacids	Z2491	Rni5	
				Rth17 à 21
55	nucleotides	Z2491	<i>Rth17</i>	
56	aminoacids	Z2491	Rth17	
57	nucleotides	Z2491	<i>rth18</i>	
58	aminoacids	Z2491	Rth18	
59	nucleotides	Z2491	<i>rth19</i>	
60	aminoacids	Z2491	Rth19	
61	nucleotides	Z2491	<i>rth20</i>	
62	aminoacids	Z2491	Rth20	
63	nucleotides	Z2491	<i>rth21</i>	
64	aminoacids	Z2491	Rth21	
				TolC Allele 1
65	nucleotides	Z2491	<i>tolC</i>	

66	aminoacids	Z2491	TolC	
67	nucleotides	Z3524	<i>tolC</i>	
68	aminoacids	Z3524	TolC	
				TolC Allele 2
69	nucleotides	Z4707	<i>tolC</i>	
70	aminoacids	Z4707	TolC	
				TolC Allele 3
71	nucleotides	Z3842	<i>tolC</i>	
72	aminoacids	Z3842	TolC	
73	nucleotides	Z4259	<i>tolC</i>	
74	aminoacids	Z4259	TolC	
75	nucleotides	Z4662	<i>tolC</i>	
76	aminoacids	Z4662	TolC	
77	nucleotides	Z4667	<i>tolC</i>	
78	aminoacids	Z4667	TolC	

79	nucleotides	Z4673	<i>tolC</i>	
80	aminoacids	Z4673	TolC	
81	nucleotides	Z4683	<i>tolC</i>	
82	aminoacids	Z4683	TolC	
83	nucleotides	Z5005	<i>tolC</i>	
84	aminoacids	Z5005	TolC	
85	nucleotides	Z6466	<i>tolC</i>	
86	aminoacids	Z6466	TolC	
87	nucleotides	Z6904	<i>tolC</i>	
88	aminoacids	Z6904	TolC	
89	nucleotides	Z7176	<i>tolC</i>	PCR oligo
90	aminoacids	Z7176	TolC	
91	nucleotidic forward primer	Z2491	<i>dsbA</i> 5' end	<i>dsbA</i>
92	nucleotidic reverse primer	Z2491	<i>dsbA</i> 5' end	

93	nucleotidic forward primer	Z2491	<i>dsbA</i> 3' end	
94	nucleotidic reverse primer	Z2491	<i>dsbA</i> 3' end	
95	nucleotidic forward primer	Z2491	<i>dsbA</i> 5' end	
96	nucleotidic reverse primer	Z2491	<i>dsbA</i> 3' end	
				Primers
97	nucleotidic forward primer	Z2491	<i>dsbA</i>	<i>dsbA</i>
98	nucleotidic reverse primer	Z2491	<i>dsbA</i>	
99	nucleotidic forward primer	Z2491	<i>fhuA</i>	<i>fhuA</i>
100	nucleotidic reverse primer	Z2491	<i>fhuA</i>	
101	nucleotidic forward primer	Z2491	<i>rniS</i>	<i>rniS</i>
102	nucleotidic reverse primer	Z2491	<i>rniS</i>	
103	nucleotidic forward primer	Z2491	<i>tolC</i>	<i>tolC</i>
104	nucleotidic reverse primer	Z2491	<i>tolC</i>	
105	nucleotidic forward primer	Z2491	<i>rth17</i>	<i>rth17</i>
106	nucleotidic reverse primer	Z2491	<i>rth17</i>	

107	nucleotidic forward primer	Z2491	<i>rth18</i>	<i>rth18</i>
108	nucleotidic reverse primer	Z2491	<i>rth18</i>	
109	nucleotidic forward primer	Z2491	<i>rth19</i>	<i>rth19</i>
110	nucleotidic reverse primer	Z2491	<i>rth19</i>	
111	nucleotidic forward primer	Z2491	<i>rth20</i>	<i>rth20</i>
112	nucleotidic reverse primer	Z2491	<i>rth20</i>	
113	nucleotidic forward primer	Z2491	<i>rth21</i>	<i>rth21</i>
114	nucleotidic reverse primer	Z2491	<i>rth21</i>	
115	nucleotidic forward primer	Z2491	<i>fhaB</i>	<i>fhaB</i>
116	nucleotidic reverse primer	Z2491	<i>fhaB</i>	



CLAIMS:

1. An isolated polypeptide comprising an amino acid sequence which has at least 70 %
5 identity to the amino acid sequence selected from the group consisting of: SEQ ID NO:2,
SEQ ID NO : 4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO : 10, SEQ ID NO : 12, SEQ
ID NO : 14, SEQ ID NO : 16, SEQ ID NO : 18, SEQ ID NO : 20, SEQ ID NO : 22, SEQ
ID NO : 24, SEQ ID NO : 26, SEQ ID NO : 28, SEQ ID NO : 30, SEQ ID NO : 32, SEQ
ID NO : 34, SEQ ID NO : 36, SEQ ID NO : 38, SEQ ID NO : 40, SEQ ID NO : 42, SEQ
10 ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ ID NO : 50, SEQ ID NO : 52, SEQ
ID NO : 54, SEQ ID NO : 56, SEQ ID NO : 58, SEQ ID NO : 60, SEQ ID NO : 62, SEQ
ID NO : 64, SEQ ID NO : 66, SEQ ID NO : 68, SEQ ID NO : 70, SEQ ID NO : 72, SEQ
ID NO : 74, SEQ ID NO : 76, SEQ ID NO : 78, SEQ ID NO : 80, SEQ ID NO : 82, SEQ
ID NO : 84, SEQ ID NO : 86, SEQ ID NO : 88, SEQ ID NO : 90.

1

2. An isolated polypeptide as claimed in claim 1 in which the amino acid sequence has at
least 95% identity to the amino acid sequence selected from the group consisting of:
SEQ ID NO:2, SEQ ID NO : 4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO : 10, SEQ ID
NO : 12, SEQ ID NO : 14, SEQ ID NO : 16, SEQ ID NO : 18, SEQ ID NO : 20, SEQ ID
20 NO : 22, SEQ ID NO : 24, SEQ ID NO : 26, SEQ ID NO : 28, SEQ ID NO : 30, SEQ ID
NO : 32, SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID NO : 38, SEQ ID NO : 40, SEQ ID
NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ ID NO : 50, SEQ ID
NO : 52, SEQ ID NO : 54, SEQ ID NO : 56, SEQ ID NO : 58, SEQ ID NO : 60, SEQ ID
NO : 62, SEQ ID NO : 64, SEQ ID NO : 66, SEQ ID NO : 68, SEQ ID NO : 70, SEQ ID
2 NO : 72, SEQ ID NO : 74, SEQ ID NO : 76, SEQ ID NO : 78, SEQ ID NO : 80, SEQ ID
NO : 82, SEQ ID NO : 84, SEQ ID NO : 86, SEQ ID NO : 88, SEQ ID NO : 90.

3. The polypeptide as claimed in claim 1 comprising the amino acid sequence selected
from the group consisting of: SEQ ID NO:2, SEQ ID NO : 4, SEQ ID NO:6, SEQ ID
30 NO:8, SEQ ID NO : 10, SEQ ID NO : 12, SEQ ID NO : 14, SEQ ID NO : 16, SEQ ID
NO : 18, SEQ ID NO : 20, SEQ ID NO : 22, SEQ ID NO : 24, SEQ ID NO : 26, SEQ ID
NO : 28, SEQ ID NO : 30, SEQ ID NO : 32, SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID
NO : 38, SEQ ID NO : 40, SEQ ID NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID

NO : 48, SEQ ID NO : 50, SEQ ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56, SEQ ID
NO : 58, SEQ ID NO : 60, SEQ ID NO : 62, SEQ ID NO : 64, SEQ ID NO : 66, SEQ ID
NO : 68, SEQ ID NO : 70, SEQ ID NO : 72, SEQ ID NO : 74, SEQ ID NO : 76, SEQ ID
NO : 78, SEQ ID NO : 80, SEQ ID NO : 82, SEQ ID NO : 84, SEQ ID NO : 86, SEQ ID
5 NO : 88, SEQ ID NO : 90.

4. An isolated polypeptide of SEQ ID NO:2, SEQ ID NO : 4, SEQ ID NO:6, SEQ ID
NO:8, SEQ ID NO : 10, SEQ ID NO : 12, SEQ ID NO : 14, SEQ ID NO : 16, SEQ ID
NO : 18, SEQ ID NO : 20, SEQ ID NO : 22, SEQ ID NO : 24, SEQ ID NO : 26, SEQ ID
10 NO : 28, SEQ ID NO : 30, SEQ ID NO : 32, SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID
NO : 38, SEQ ID NO : 40, SEQ ID NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID
NO : 48, SEQ ID NO : 50, SEQ ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56, SEQ ID
NO : 58, SEQ ID NO : 60, SEQ ID NO : 62, SEQ ID NO : 64, SEQ ID NO : 66, SEQ ID
NO : 68, SEQ ID NO : 70, SEQ ID NO : 72, SEQ ID NO : 74, SEQ ID NO : 76, SEQ ID
15 NO : 78, SEQ ID NO : 80, SEQ ID NO : 82, SEQ ID NO : 84, SEQ ID NO : 86, SEQ ID
NO : 88, SEQ ID NO : 90.

5. An immunogenic fragment of the polypeptide as claimed in any one of claims 1 to 4 in
which the immunogenic activity of said immunogenic fragment is substantially the same
20 as the polypeptide of SEQ ID NO:2, SEQ ID NO : 4, SEQ ID NO:6, SEQ ID NO:8, SEQ
ID NO : 10, SEQ ID NO : 12, SEQ ID NO : 14, SEQ ID NO : 16, SEQ ID NO : 18, SEQ
ID NO : 20, SEQ ID NO : 22, SEQ ID NO : 24, SEQ ID NO : 26, SEQ ID NO : 28, SEQ
ID NO : 30, SEQ ID NO : 32, SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID NO : 38, SEQ
ID NO : 40, SEQ ID NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ
25 ID NO : 50, SEQ ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56, SEQ ID NO : 58, SEQ
ID NO : 60, SEQ ID NO : 62, SEQ ID NO : 64, SEQ ID NO : 66, SEQ ID NO : 68, SEQ
ID NO : 70, SEQ ID NO : 72, SEQ ID NO : 74, SEQ ID NO : 76, SEQ ID NO : 78, SEQ
ID NO : 80, SEQ ID NO : 82, SEQ ID NO : 84, SEQ ID NO : 86, SEQ ID NO : 88, SEQ
ID NO : 90.

30

6. An isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide that
has at least 70% identity to the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14,
16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62,

64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, or 100 over the entire length of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90 respectively; or a nucleotide sequence complementary to said isolated polynucleotide.

7. An isolated polynucleotide comprising a nucleotide sequence that has at least 70% identity to a nucleotide sequence encoding a polypeptide of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, or 90 over the entire coding region; or a nucleotide sequence complementary to said isolated polynucleotide.

8. An isolated polynucleotide which comprises a nucleotide sequence which has at least 70% identity to that of SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89 over the entire length of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89 respectively; or a nucleotide sequence complementary to said isolated polynucleotide.

9. The isolated polynucleotide as claimed in any one of claims 6 to 8 in which the identity is at least 95% to SEQ ID NO : 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, or 89.

10. An isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2, SEQ ID NO : 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO : 10, SEQ ID NO : 12, SEQ ID NO : 14, SEQ ID NO : 16, SEQ ID NO : 18, SEQ ID NO : 20, SEQ ID NO : 22, SEQ ID NO : 24, SEQ ID NO : 26, SEQ ID NO : 28, SEQ ID NO : 30, SEQ ID NO : 32, SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID NO : 38, SEQ ID NO : 40, SEQ

ID NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ ID NO : 50, SEQ
ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56, SEQ ID NO : 58, SEQ ID NO : 60, SEQ
ID NO : 62, SEQ ID NO : 64, SEQ ID NO : 66, SEQ ID NO : 68, SEQ ID NO : 70, SEQ
ID NO : 72, SEQ ID NO : 74, SEQ ID NO : 76, SEQ ID NO : 78, SEQ ID NO : 80, SEQ
5 ID NO : 82, SEQ ID NO : 84, SEQ ID NO : 86, SEQ ID NO : 88, SEQ ID NO : 90.

11. An isolated polynucleotide comprising the polynucleotide of SEQ ID NO : 1, SEQ ID
NO : 3, SEQ ID NO : 5, SEQ ID NO : 7, SEQ ID NO : 9, SEQ ID NO : 11, SEQ ID NO :
13, SEQ ID NO : 15, SEQ ID NO : 17, SEQ ID NO : 19, SEQ ID NO : 21, SEQ ID NO :
10 23, SEQ ID NO : 25, SEQ ID NO : 27, SEQ ID NO : 29, SEQ ID NO : 31, SEQ ID NO :
33, SEQ ID NO : 35, SEQ ID NO : 37, SEQ ID NO : 39, SEQ ID NO : 41, SEQ ID NO :
43, SEQ ID NO : 45, SEQ ID NO : 47, SEQ ID NO : 49, SEQ ID NO : 51, SEQ ID NO :
53, SEQ ID NO : 55, SEQ ID NO : 57, SEQ ID NO : 59, SEQ ID NO : 61, SEQ ID NO :
63, SEQ ID NO : 65, SEQ ID NO : 67, SEQ ID NO : 69, SEQ ID NO : 71, SEQ ID NO :
15 73, SEQ ID NO : 75, SEQ ID NO : 77, SEQ ID NO : 79, SEQ ID NO : 81, SEQ ID NO :
83, SEQ ID NO : 85, SEQ ID NO : 87, SEQ ID NO : 89.

12. An isolated polynucleotide comprising a nucleotide sequence encoding the polypeptide
of SEQ ID NO:2, SEQ ID NO : 4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO : 10, SEQ
20 ID NO : 12, SEQ ID NO : 14, SEQ ID NO : 16, SEQ ID NO : 18, SEQ ID NO : 20, SEQ
ID NO : 22, SEQ ID NO : 24, SEQ ID NO : 26, SEQ ID NO : 28, SEQ ID NO : 30, SEQ
ID NO : 32, SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID NO : 38, SEQ ID NO : 40, SEQ
ID NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ ID NO : 50, SEQ
ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56, SEQ ID NO : 58, SEQ ID NO : 60, SEQ
25 ID NO : 62, SEQ ID NO : 64, SEQ ID NO : 66, SEQ ID NO : 68, SEQ ID NO : 70, SEQ
ID NO : 72, SEQ ID NO : 74, SEQ ID NO : 76, SEQ ID NO : 78, SEQ ID NO : 80, SEQ
ID NO : 82, SEQ ID NO : 84, SEQ ID NO : 86, SEQ ID NO : 88, or SEQ ID NO : 90,
obtainable by screening an appropriate library under stringent hybridization conditions with a
labeled probe having the sequence of SEQ ID NO : 1, SEQ ID NO : 3, SEQ ID NO : 5, SEQ
30 ID NO : 7, SEQ ID NO : 9, SEQ ID NO : 11, SEQ ID NO : 13, SEQ ID NO : 15, SEQ ID NO

: 17, SEQ ID NO : 19, SEQ ID NO : 21, SEQ ID NO : 23, SEQ ID NO : 25, SEQ ID NO : 27, SEQ ID NO : 29, SEQ ID NO : 31, SEQ ID NO : 33, SEQ ID NO : 35, SEQ ID NO : 37, SEQ ID NO : 39, SEQ ID NO : 41, SEQ ID NO : 43, SEQ ID NO : 45, SEQ ID NO : 47, SEQ ID NO : 49, SEQ ID NO : 51, SEQ ID NO : 53, SEQ ID NO : 55, SEQ ID NO : 57, SEQ ID NO : 59, SEQ ID NO : 61, SEQ ID NO : 63, SEQ ID NO : 65, SEQ ID NO : 67, SEQ ID NO : 69, SEQ ID NO : 71, SEQ ID NO : 73, SEQ ID NO : 75, SEQ ID NO : 77, SEQ ID NO : 79, SEQ ID NO : 81, SEQ ID NO : 83, SEQ ID NO : 85, SEQ ID NO : 87, or SEQ ID NO : 89, or a fragment thereof.

10 13. An expression vector or a recombinant live microorganism comprising an isolated polynucleotide according to any one of claims 6-12.

14. A host cell comprising the expression vector of claim 13 or a membrane of said host cell expressing an isolated polypeptide comprising an amino acid sequence that has at least 70% identity to the amino acid sequence selected from the group consisting of :
15 SEQ ID NO:2, SEQ ID NO : 4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO : 10, SEQ ID NO : 12, SEQ ID NO : 14, SEQ ID NO : 16, SEQ ID NO : 18, SEQ ID NO : 20, SEQ ID NO : 22, SEQ ID NO : 24, SEQ ID NO : 26, SEQ ID NO : 28, SEQ ID NO : 30, SEQ ID NO : 32, SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID NO : 38, SEQ ID NO : 40, SEQ ID NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ ID NO : 50, SEQ ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56, SEQ ID NO : 58, SEQ ID NO : 60, SEQ ID NO : 62, SEQ ID NO : 64, SEQ ID NO : 66, SEQ ID NO : 68, SEQ ID NO : 70, SEQ ID NO : 72, SEQ ID NO : 74, SEQ ID NO : 76, SEQ ID NO : 78, SEQ ID NO : 80, SEQ ID NO : 82, SEQ ID NO : 84, SEQ ID NO : 86, SEQ ID NO : 88, or SEQ ID NO : 90.

25

15. A process for producing a polypeptide comprising an amino acid sequence that has at least 70% identity to the amino acid sequence selected from the group consisting of:
SEQ ID NO:2, SEQ ID NO : 4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO : 10, SEQ ID NO : 12, SEQ ID NO : 14, SEQ ID NO : 16, SEQ ID NO : 18, SEQ ID NO : 20, SEQ ID NO : 22, SEQ ID NO : 24, SEQ ID NO : 26, SEQ ID NO : 28, SEQ ID NO : 30, SEQ ID NO : 32, SEQ ID NO : 34, SEQ ID NO : 36, SEQ ID NO : 38, SEQ ID NO : 40, SEQ ID

NO : 42, SEQ ID NO : 44, SEQ ID NO : 46, SEQ ID NO : 48, SEQ ID NO : 50, SEQ ID NO : 52, SEQ ID NO : 54, SEQ ID NO : 56, SEQ ID NO : 58, SEQ ID NO : 60, SEQ ID NO : 62, SEQ ID NO : 64, SEQ ID NO : 66, SEQ ID NO : 68, SEQ ID NO : 70, SEQ ID NO : 72, SEQ ID NO : 74, SEQ ID NO : 76, SEQ ID NO : 78, SEQ ID NO : 80, SEQ ID NO : 82, SEQ ID NO : 84, SEQ ID NO : 86, SEQ ID NO : 88, or SEQ ID NO : 90 comprising culturing a host cell of claim 18 under conditions sufficient for the production of said polypeptide and recovering the polypeptide from the culture medium.

10 16. A process for expressing a polynucleotide of any one of claims 6 – 12 comprising transforming a host cell with the expression vector comprising at least one of said polynucleotides and culturing said host cell under conditions sufficient for expression of any one of said polynucleotides.

15 17. A vaccine composition comprising an effective amount of the polypeptide of any one of claims 1 to 5 and a pharmaceutically acceptable carrier.

18. A vaccine composition comprising an effective amount of the polynucleotide of any one of claims 6 to 12 and a pharmaceutically effective carrier.

20 19. The vaccine composition according to either one of claims 17 or 18 wherein said composition comprises at least one other *Neisseria meningitidis* antigen.

20. An antibody immunospecific for the polypeptide or immunological fragment as claimed in any one of claims 1 to 5.

25

21. A method of diagnosing a *Neisseria* infection, comprising identifying a polypeptide as claimed in any one of claims 1 - 5, or an antibody that is immunospecific for said polypeptide, present within a biological sample from an animal suspected of having such an infection.

22. Use of a composition comprising an immunologically effective amount of a polypeptide as claimed in any one of claims 1 – 5 in the preparation of a medicament for use in generating an immune response in an animal.

5

23. Use of a composition comprising an immunologically effective amount of a polynucleotide as claimed in any one of claims 6 - 12 in the preparation of a medicament for use in generating an immune response in an animal.

10 24. A therapeutic composition useful in treating humans with *Neisseria meningitidis* disease comprising at least one antibody directed against the polypeptide of claims 1 – 5 and a suitable pharmaceutical carrier.

ABSTRACT OF THE DISCLOSURE

- 5 The invention provides novel *Neisseria meningitidis* (Nm) polypeptides and polynucleotides which cover the Nm genetic diversity, and which correspond to polypeptide of Nm outer membrane and/or periplasma, and to methods for producing such Nm compounds. Also provided are anti-Nm infection, and particularly diagnostic, prophylactic and therapeutic uses thereof.

10

FIGURE 1A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC
151 TAACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA
● 1 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC
1 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGCTCAA ATGGAAGAGT

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ACCAATAA ATCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 1A (suite)

FIGURE 1B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 2A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC

51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA

101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC

151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA

201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC

251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC

301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC

351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT

401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG

451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC

501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGCTCAA ATGGAAGAGT

551 TACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TCTCGGCGGC

601 AAATACCAAG TTGAATTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 2A (suite)

FIGURE 2B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVWVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 3A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC

51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA

101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC

151 TAACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA

201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC

251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC

301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC

351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT

401 TCGATGCGAT GGTAAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG

451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC

501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TGCGGCTCAA ATGGAAGAGT

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DRAW

GACCAATAA A CAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 3A (suite)

FIGURE 3B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 4A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TGCGGCTCAA ATGGAAGAGT

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 4A (suite)

FIGURE 4B

1 MKLKTALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 5A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA
1 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC
● 1 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TGCGGCTCAA ATGGAAGAGT

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551 CACCAATAA ATCAAATC ACCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 5A (suite)

FIGURE 5B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 6A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC

51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA

101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC

151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA

201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC

251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC

301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC

351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT

401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG

451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC

501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGCTCAA ATGGAAGAGT

ACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT TGTGCGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 6A (suite)

FIGURE 6B

1 MKLKTALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 7A

1 ATGAAACTGA AACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC
51 CGCTTGTAGC AACACGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AACCTTTGG CACGTTTGGC
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGGCTCAA ATGGAAGAGT

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551 TACCAATAA ATTCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 7A (suite)

FIGURE 7B

1 MKLKTALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 8A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC
151 TACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGCTCAA ATGGAAGAGT

601 AAATACCAAG TTGAATTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 8A (suite)

FIGURE 8B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 9A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC

51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA

101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC

151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA

201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC

251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC

301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC

351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT

401 TCGATGCGAT GGTAAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG

451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC

501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TGCGGCTCAA ATGGAAGAGT

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ACCAATAA ATTAAATC ACCGGCACAC CGACTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTAA AGACTGGCAG TCTGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 9A (suite)

FIGURE 9B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIPQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 10A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC
51 CGCTTGTAGC AAACAGGCTG AAACCAGTGT TCCGGCAGAC AGCGCCCAAA
101 GCAGCTCATC TGCTCCGGCA GCCCCTGCTG AGTTGAACGA AGGTGTGAAC
151 TACACTGTAT TGTCTACGCC TATTCCGCAA CAGCAGGCCG GTAAAATCGA
201 AGTATTGGAA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC
501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGGCTCAA ATGGAAGAGT

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCTGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 10A (suite)

FIGURE 10B

1 MKLKTALTS LTLLALAACS KQAETSVPAD SAQSSSSAPA APAELNEGVN

51 YTVLSTPIQ QQAGKIEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 11A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC

51 CGCTTGTAGC AAACAGGCTG AAACCAGCGT TCCGGCAGAC AGCGTCCAAA

101 GCAGCTCATC TGCTCCGGCA GCCCCAGCCC CATTGACCGA AGGCGTGAAC

151 TAACTGTAT TGTCCACGCC TATCCCGCAA CAGCAGGCCG GCAAAGTCGA

201 AGTCTTGGA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC

251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC

301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC

351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT

401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG

451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC

501 TGCATTTGAG GCTTCTGAAA GCCAAGCGCG TCGGCTCAA ATGGAAGAGT

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DRAW

551 TGACCAATAA ATTCCAAATC AGCGGCACAC CGACTGTGAT CGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 11A (suite)

FIGURE 11B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SVQSSSSAPA APAPLTEGVN

51 YTVLSTPIPQ QQAGKVEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE ASESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 12A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC
51 CGCTTGTAGC AAACAGGCTG AAACCAGCGT TCCGGCAGAC AGCGTCCAAA
101 GCAGCTCATC TGCTCCGGCA GCCCCAGCCC CATTGACCGA AGGCGTGAAC
151 TAACTGTAT TGTCCACGCC TATCCCGCAA CAGCAGGCCG GCAAAGTCGA
201 AGTCTTGGA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC
251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC
301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC
351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT
401 TCGATGCGAT GGTTAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG
451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC
501 TGCATTTGAG GCTTCTGAAA GCCAAGCGCG TCGGCTCAA ATGGAAGAGT

...ACCAATAAATTCCAAATC ACCGCGGCGGCGACTGTGAT CGTCGGCGGC

601 AAATACCAAG TTGAATTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 12A (suite)

FIGURE 12B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SVQSSSSAPA APAPLTEGVN

51 YTVLSTPIPQ QQAGKVEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE ASESQARAAQ MEELTNKFQI SGTPTVIVGG

201 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

FIGURE 13A

1 ATGAAACTGA AAACCTTAGC TTTGACTTCA TTGACCCTGT TGGCATTGGC

51 CGCTTGTAGC AAACAGGCTG AAACCAGCGT TCCGGCAGAC AGCGTCCAAA

101 GCAGCTCATC TGCTCCGGCA GCCCCAGCCC CATTGACCGA AGGCGTGAAC

151 TAACTGTAT TGTCCACGCC TATCCCGCAA CAGCAGGCCG GCAAAGTCGA

201 AGTCTTGGA TTTTTCGGCT ACTTCTGCCC GCATTGCGCC CATCTTGAGC

251 CGGTCTTGAG CGAGCACATC AAAACGTTTA AAGACGATAC CTATATGCGC

301 CGGGAGCATG TCGTGTGGGG TGATGAAATG AAACCTTTGG CACGTTTGGC

351 GGCCGCAGTG GAAATGGCCG GTGAATCAGA TAAAGCCAAC AGCCATATTT

401 TCGATGCGAT GGTAAATCAA AAAATCAATC TGGCCGATAC CGATACCCTG

451 AAAAAATGGC TGTCCGAGCA AACAGCGTTT GACGGCAAAA AAGTATTGGC

501 TGCATTTGAG GCTCCTGAAA GCCAAGCGCG TCGGGCTCAA ATGGAAGAGT

ACCAATAA ATTCAAATC AGCGGCACAC CGACTGTGAT TGTCGGCGGC

601 AAATACCAAG TTGAATTTAA AGACTGGCAG TCCGGTATGA CCACGATTGA

651 CCAGTTGGTG GATAAAGTAC GCGAAGAGCA GAAAAAGCCG CAATAA

FIGURE 13A (suite)

FIGURE 13B

1 MKLKTLALTS LTLLALAACS KQAETSVPAD SVQSSSSAPA APAPLTEGVN

51 YTVLSTPIPQ QQAGKVEVLE FFGYFCPHCA HLEPVLSEHI KTFKDDTYMR

101 REHVVGDEM KPLARLAAAV EMAGESDKAN SHIFDAMVNQ KINLADTDTL

151 KKWLSEQTAF DGKKVLAAFE APESQARAAQ MEELTNKFQI SGTPTVIVGG

● 1 KYQVEFKDWQ SGMTTIDQLV DKVREEQKKP Q*

Z2491, *fhaB*Figure 14A

1 GAGTATGCTC TTAGAGAAAA ATTGATCAAA AAAGCCAAAG GGAAAGGCCT
51 ATTATCTTTA GATTGGGGCA GCCTGACCGA ACAAGAGGCA AGGCAGTTTA
101 TCTATTTGAT TGAGAAAGAT CGATATTCTA ATCAATTGCT TGACCGATAT
151 CAAAAAATC CAAGTAGTTT AAATAATCAA GAAAAAATA TTCTTGCATA
201 TTTTATTAAC CAAACCTCTG GAGGTAACAC AGCTTGGGCA GCTTCGATAC
251 TGAAAACGCC CCAGTCAATG GGTAATCTCA CTATTCCTTC CAAAGATATT
301 AATAACACCT TATCGAAAGC CTATCAAACA TTGAGTCGTT ATGATTCTTT
351 TGATTACAAA TCAGCTGTTG CCGCACAACC TGCACTTTAC TTATTAAACG
401. GACCGCTTGG CTTCAGTGTC AAAGCAGCTA CTGTGGCAGC AGGAGGATAT
451 AACATTGGAC AGGGAGCGAA AGCAATCTCT AATGGAGAAT ATCTGCATGG
501 TACAGTTCAG GTTGTTAATG GCACATTGAT GGTTCAGGA TCTGTATCTG
551 CACAGGCTGC AATATCGGCC AAGCCTGCAC CTGTTACCCG TTATCTGAGC
601 AATGACAGTG CTCCTGCTTT AAGACAAGCT TTAAGTGCTG AAAGCCAGAG
651 AATCCGCATG AAAGTCCGG AAGAGTATCG ACAAATAGGG AATCTTGCGA
701 TAGCAAAAAT TGATGTAAA GGATTACCGC AAAGGATGGA AGCATTTAGT

751 TCTTTCCAAA AAGGGGAACA TGGATTTATT TCGTTACCTG AAACAAAAAT
801 TTTTAAACCT ATATCTGTTG ATAAATATCA TAATATTGCC TCTCCTCCTA
851 GAGGAACATT AAGAAATATA GATGGAGAAT ATAAATTACT TGAAACTATA
901 GCACAGCAAC TCGGAAATAA TCGTAATGTA TCAGGTAGAA TTGATCTATT
951 TACAGAATTA AAGGCCTGTC AATCTTGCAG CAATGTTATT TTAGAGTTTA
1001 GAAATCGCTA TCCAAATATT CAATTAAATA TTTTACAGG AAAATAG

Figure 14A (suite)

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Z2491, FhaB

Figure 14B

1 EYALREKLIK KAKGKGLLSL DWGSLTEQEA RQFIYLIEKD RYSNQLLDRY
51 QKNPSSLNNQ EKNILAYFIN QTSGGNTAWA ASILKTPQSM GNLTIPSKDI
101 NNTLSKAYQT LSRYSDFDYK SAVAAQPALY LLNGPLGFSV KAATVAAGGY
151 NIGQGAKAIS NGEYLHGTVQ VVNGTLMVAG SVSAQAAISA KPAPVTRYLS
201 NDSAPALRQA LTAESQRIRM KLPEEYRQIG NLAIKIDVK GLPQRMEAFS
251 SFQKGEHGF I SLPETKIFKP ISVDKYHNIA SPPRGTLRNI DGEYKLLET I
301 AQQLGNNRNV SGRIDLFTL KACQSCSNVI LEFRNRY PNI QLNIFTGK

FIGURE 15A

1 ATGAAAATAT CATTTCAATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGGCGAA AGCATTTTCC TCGCGGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GCGGGCGGTG TCATCAACAT
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT

551 ATGGTTCGTG GGCAACCGC AGCCIGAATA TGGACATCAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCCGACTG CTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTC

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

1151 TTTCCGCCTC CATCAACCGT TACGACCGCG CAAGCTGGCC GCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTC AACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC

1801 CGAGTGGGCA TCCATTGAA TAACACCAGC AACGTTACCG GCAACCTGTT

1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGC GTAACCG

1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG

1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA

2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC

2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT

2101 TACCGTTTCT GA

FIGURE 15A (suite 3)

1 MKISFHLALL PTLIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLLSSNLT

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTL

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT

651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN

701 YRF*

FIGURE 15B (suite)

FIGURE 16A

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGCGCGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GGCGGCGGTG TCATCAACAT
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT

551 ATGGTTCGTG GGCAACCGC AGCCIGAATA TGGACATCAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCCGACTG CTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

1151 TTTCCGCCTC CATCAACCC TACGACCGCG CAAGCTGGCC GCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAA ACTCTA TCTGCGCGGT

1751 TCGTTGGGCG TGATGCAGGC GAAAGTCGTT GAAGACAAAG AAAATCCCGA

1801 CCGAGTGGGC ATCCATTTGA ATAACACCAG CAACGTTACC GGCAACCTGT

1851 TTTTCCGTTA TACCCCGACC GAAAACCTCT ACGGCGAAAT CGGCGTAACC

1901 GGTACAGGCA AACGCTACGG TTACGACTCA AGAAATAAAG AAGTGACTAC

1951 GCTTCCAGGC TTGCCCCGAG TTGATGCCAT GCTTGGCTGG AACCATAAAA

2001 ATGTTAACGT TACCTTTGCC GCAGCCAATC TGTTCATCA AAAATATTGG

2051 CGTTCGGACT CTATGCCGGG TAATCCGCGC GGCTATACTG CCCGGGTAAA

2101 TTACCGTTTC TGA

FIGURE 16A (suite 3)

FIGURE 16B

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNLTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

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DRAW

551 NPYYAVSGK HRSRVELSA IGQIPKKTL SARFVGRDAG ESR*RQRKSR

601 PSGHPFE*HQ QRYRQPVFPL YPDRKPLRRN RRNRYRQTLR LRLKK*RSY

651 ASRLCPS*CH AWLEP*KC*R YLCRSQSVQS KILAFGLYAG *SARLYCPGK

701 LPFL

FIGURE 16B (suite)

FIGURE 17A

1 ATGAAAATAT CATTTCA TTT AGCTTTATTA CCCACGCTGA TTATTGCTTC

51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG

101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC

151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT

201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA

251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC

301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TCGCGGTTTT

351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC

401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT TCTGAAAGGC

451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GGCGGTGGCG TCATCAACAT

501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGAGCGGTTT

551 ACGGCTCAAG GGCAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTGGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA TTTCACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCATTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC CTTAGGTTAC AGCCGCGCCT

1151 TTACTGCTTC CATCGATCCTTACGACCGAG CAAGCTGGCC CCTTCGGGC

1201 AGATTGCAGC CTATCCTCAC CAAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAGTACAG CGGCCACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAACCCCG TTCACACACT TTACGCCTCG TATAACAAAG

1451 GTTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTCA

1501 TCTTCTGCCG TGTTTAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTCAAA AGCAGTTGGC TGGACAATCG TTTGGACACC ACATTGTCCG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGA CGCGGAAAAT

1651 AATCCCTACA CTTGGGCAGT CGGCGGCAAA CACCGTTCGC GTGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAAA AAATCCCGAC

1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT

1851 TTTCCGTTAT ACCCGACCGA AAACCTCTAC GCGGAAATCG GCGTAACCGG

1901 TACAGGCAAA CGCTACGGTT ACAACTCAAG AAATAAAGAA GTGACTACGC

1951 TTCCAGGCTT TGCCCGAGTT GATGCCATGC TTGGCTGGAA CCATAAAAAT

2001 GTTAACGTTA CCTTTGCCGC AGCCAATCTG TTCAATCAAA AATATTGGCG

2051 TTCGGACTCT ATGCCGGGTA ATCCGCGCGG CTATACTGCC CGGGTAAATT

2101 ACCGTTTCTG A

FIGURE 17A (suite 3)

1 MKISFHLALL PTLIIASFPV AAADTQDNGE IYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVS K YANFKQSRNI GAVYGSRANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNFTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY SRAFTASIDP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTS

501 SSAVFNADPE YTRQYETGVK SSWLDNRLDT TLSAYQIERF NIRYRPDAEN

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DRAW

551 NPTWAVGGK HRS VLSA IGQPRKET ERGSLGVMQY KVVEDKKNP

601 RVGIHLNNTS NVTGNLFFRY TRPKTSTAKS A*PVQANATV TTQEIKK*LR

651 FQALPELMPC LAGTIKMLTL PLPQPICSIK NIGVRTLCRV IRAAILPG*I

701 TVS

FIGURE 17B (suite)

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC

51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG

101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC

151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT

201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA

251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC

301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGC GCGGTTT

351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC

401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC

451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GGCGGCGGCG TCATCAACAT

501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGAGCGGTTT

551 ACGGCTCATG GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAAC TCGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACGCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGTCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAATAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CAACACGTGCG

1501 TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGTGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA CGAGCAAAAT

1651 GATCCCTACA CTTGGGCAGT CGGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC

1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT

1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCGTAACCG

1901 GTACAGGCAA ACGCTACGGT TACAACCTCAA GAAATAAAGA AGTGACTACG

1951 CTTCCAGGCT TTGCCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA

2001 TGTTAACATT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC

2051 GTTCGGATGC CATGCCCCGGC GCGCCGCGCA CTTATACGGC GCGGGTTAAT

2101 TACAGTTTCT AA

FIGURE 18A (suite 3)

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSSNLTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG

401 RLQPILTQNR HKADAYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSINTS

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDEQN

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DRAW

331 DPTWAVGGK HRSKVELSA IGQIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNI TFAAANLLNQ KYWRSDAMPG APRTYTARVN

701 YSF*

FIGURE 18B (suite)

1 ATGAAAATAT CATTTCAATT AGCTTTATTA CCCACGCTGA TTATTGCTTC

51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG

101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC

151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT

201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC TAGAAAAACA

251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC

301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGCGCGGTTT

351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC

401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC

451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGGCGGCG TCATCAACAT

501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

551 ACGGTTTCGTG GGCAACCGC AGCCTGAATA TGGACATTAA CGAAGTGTTG

601 AACAAAAACG TCGCCATCCG TCTCACC GGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCCG CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTGGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGCTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA TTTCACGCTA

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCATTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC CTTAGGTTAC AGCCGCGCCT

1151 TTACTGCTTC CATCGATC TACGACCGAG CAAGCTGGCC GCTTCGGGC

1201 AGATTGCAGC CTATCCTCAC CAAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGTCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAATAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CAACACGTCTG

1501 TCTTCCGCCG TGTTC AACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGTGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA CGAGCAAAAT

1651 GATCCCTACA CTTGGGCAGT CGGCGGCAAA CACCGTTCGC GCGGCGTGGA

701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC

1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT

1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG

1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG

1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA

2001 TGTTAACATT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC

2051 GTTCGGATGC CATGCCCGGC GCGCCGCGCA CTTATACGGC GCGGGTTAAT

2101 TACAGTTTCT AA

FIGURE 19A (suite 3)

FIGURE 19B

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI *KNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNFTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY SRAFTASIDP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSINTS

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDEQN

551 DPYTWAVGGK HRSRGVELSA IGQIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNI TFAAANLLNQ KYWRSDAMPG APRTYTARVN

701 YSF*

FIGURE 19B (suite)

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC

51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG

101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC

151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT

201 CATCAAAGAA ACGCCGCAA CCATCGATAC GCTCAATATC TAGAAAAACA

251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC

301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGC GCGGTTT

351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC

401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC

451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGGCGGCG TCATCAACAT

501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

551 ACGGTTTCGTG GGCAACCGC AGCCTGAATA TGGACATTAA CGAAGTGTTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTGGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGCTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA TTTCACGCTA

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCCTTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGCTAC CGCGGCAGTT

1151 TCACCGTGCC CATCAACC TACGACCGCG CAAGCTGGCC CTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCTAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAACAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAACCCAG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGTAT CGATACGTTG

1501 TCTTCCGCCG TGTTC AACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACC ACATTGTCCG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC

1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT

1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG

1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG

1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA

2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC

2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT

2101 TACCGTTTCT GA

FIGURE 20A (Suite 3)

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI *KNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKVDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSSNFTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY RGSFTVPINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFMLGGRYDK YTFNSENKLT

451 GNSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGAFAPYGG RGGYLSIDTL

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

551 NF IYAVSGK HRS VLSA IGQIPKKLY LRGSLGVM KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN

701 YRF*

FIGURE 20B (suite)

FIGURE 21A

1 ATGAAAATAT CATTTCA TTT AGCTTTATTA CCCACGCTGA TTATTGCTTC

51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG

101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC

151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT

201 CATCAAAGAA ACGCCGCAA CCATCGATAC GCTCAATATC CAGAAAAACA

251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC

301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGCGCGGTTT

351 TCAAGCCGAC GCATCCGATA TTTACGCGA CGGCGTGCGC GAAAGCGGAC

401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC

451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGGCGGCG TCATCAACAT

501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

551 ACGGTTAGTG GGAACCGC AGCCIGAATA TGGAATAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTGGGACTG CTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTC

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC

1001 ACGCCTGGCA GCAGACTGAC AACAAAACCC TGTCGTCCAA TTTCACGCTA

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACTTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC CTTAGGTTAC AACCGCGCCT

1151 TTTCCGCCTC CATCAAC TACGACCGCG CAAGCTGGCC CTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CAAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC

1651 AACCCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCTAA AAAACTCTAT CTGCGCGGTT

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC

1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT

1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGC GTAACCG

1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGT GACTACG

1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA

2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC

2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT

2101 TACCGTTTCT GA

FIGURE 21A (suite 3)

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYG*WANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNFTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY NRAFSASINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFMLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGAFAPYGG RGGYLSIDTL

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

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DRAW

551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT

651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN

701 YRF*

FIGURE 21B (suite)

1 ATGAAAATAT CATTTCAATT AGCTTTATTA CCCACGCTGA TTATTGCTTC

51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG

101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC

151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT

201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA

251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC

301 ATCGACGCTG CCTACGATAT GCGCGGTGAA AGCATTTTCC TGC GCGGTTT

351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC

401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC

451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGCGGGC TCATCAACAT

501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

551 ACGGTTTCGTG GGCACACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCCGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGT CGCGAACACC GCAACCCGAC ATTGGGCTAC CGCGGCAGTT

1151 TCACCGTGCC CATCAACCC TACGACCGCG CAAGCTGGCC GCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCTAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAACAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAACCCAG TCCACACACT TTATGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCTATT TGAGTATCGA CACTTCGTCT

1501 GCCGCCGTGT TCAACGCCGC CCCCAGGTAC ACTCGCCAAT ACGAAACCGG

1551 TGTGAAAAGC AGTTGGCTGG ACGACCGCCT CAGCACCACA TTGTCCGCCT

1601 ACCAAATCGA ACGCTTCAAT ATCCGCTACC GCCCGATCC AAAAAACAAC

1651 CCTTATATTT ATGCGGTTAG CGGCAAACAC CGTTCGCGCG GCGTGGAATT

1701 GTCCGCCATC GGGCAAATCA TCCCTAAAAA ACTCTATCTG CGCGGTTCTG

1751 TGGGCGTGAT GCAGGCGAAA GTCGTTGAAG ACAAAGAAAA TCCCGACCGA

1801 GTGGGCATCC ATTTGAATAA CACCAGCAAC GTTACCGGCA ACCTGTTTTT

1851 CCGTTATACC CCGACTGAAA ACCTCTACGG CGAAATCGGC GTAACCGGTA

1901 CAGGCAAACG CTACGGCTAC AACTCAAGAA ATAAAGAAGT GACCACGCTT

1951 CCAGGCTTTG CCCGAGTTGA TGCCATGCTC GGCTGGAACC ATAAAAATGT

2001 TAACGTTACC TTTGCCGCTG CCAATCTGCT CAATCAAAAA TATTGGCGTT

2051 CGGACTCTAT GCCGGGTAAT CCGCGCGGCT ATACTGCCCG GGTAATTAC

2101 CGTTTCTGA

FIGURE 22A (suite 3)

FIGURE 22B

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSSNLTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY RGSFTVPINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFNSENKLT

451 GNSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGYLSIDTSS

501 AAVFNAAPEY TRQYETGVKS SWLDDRLSTT LSAYQIERFN IRYRPDPKNN

551 PYIYAVSGKH RS

ELSAI GQIIPKKLYL RGS LGVM

VVEDKENPDR

601 VGIHLNNTSN VTGNLFFRYT PTENLYGEIG VTGTGKRYGY NSRNKEVTTL

651 PGFARVDAML GWNHKNVNVF FAAANLLNQK YWRSDSMPGN PRGYTARVNY

701 RF*

FIGURE 22B (suite)

1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC

51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG

101 CCACGCTACC TACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC

151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT

201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA

251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC

301 ATCGACGCTG CCTACGATAT GCGCGGTGAA AGCATTTTCC TGCGCGGTTT

351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC

401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC

451 CCGTCTTCCG TGCTTTACGG CCGTACCAAC GCGGGCGGCG TCATCAACAT

501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

551 ACGGTTTCGTG GG AACCGC AGCCTGAATA TGGA TAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACCT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCCGACTG CTTACCGCA TGGGGTTCGC CCACCCGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TCGAATACGC CTTCAACGAC

901 AAATGGCGCG CCCAATGGCA GCTCGCCCAC CGCACGGCAG CGCAGGATTT

951 CGACCATTTT TATGCAGGCA GCGAAAACGG CAGCCGAATC AAACGCAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCTC TGTCGTCCAA CTTACGCTC

1051 AACGGCGACT ACACCATCGG TCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGCTAC CGCGGCAGTT

1151 TCACCGTGCC CATCAAC TACGACCGCG CAAGCTGGCC GCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAAACATCT TCTCCGCTAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAACAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAACCCAG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGATATT TGAGTATCGA CACTTCGTCT

1501 GCCGCCGTGT TCAACGCCGC CCCCAGGTAC ACCCCCAATA CGAAACCGGC

1551 GTCAAAAGCA GTTGGCTGGA CAATCGTTTG GACACCACCC TGTCGGTTTA

1601 CCAAATCGAA CGCTTCAATA TCCGCTACCG CCCCAGTCCA AAAACAACC

1651 CTTATATTTA TGCGGTTAGC GGCAAACACC GTTCGCGCGG CGTGGAATTG

1701 TCCGCCATCG GGCAAATCAT CCCCAAAAAA CTCTATCTGC GCGGTTTCGTT

1751 GGGCGTGATG CAGGCGAAAG TCGTTGAAGA CAAAGAAAAT CCCGACCGAG

1801 TGGGCATCCA TTTGAATAAC ACCAGCAACG TTACCGGCAA CCTGTTTTTC

1851 CGTTATACCC CGACCGAAAA CCTCTACGGC GAAATCGGCG TAACCGGTAC

1901 GGGCAAACGC TACGGTTACA ACTCAAGAAA TAAAGAAGTG ACTACGCTTC

1951 CAGGCTTTGC CCGAGTTGAT GCCATGCTTG GCTGGAACCA TAAAAATGTT

2001 AACGTTACCT TTGCCGCAGC CAATCTGTTC AATCAAAAAT ATTGGCGTTC

2051 GGACTCTATG CCGGGTAATC CGCGCGGCTA TACTGCCCGG GTAAATTACC

2101 GTTTCTGA

FIGURE 23A (suite 3)

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHPN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGSRI KRNYAWQQTD NKTLSNFTL
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY RGSFTVPINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFENSENKL
451 GNSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGYLSIDTSS
501 AAVFNAAPEY TPNTKPASKA VGWTIVWTPP CRFTKSNASI SATAPIQKTT

551 LIFMRLAANT VR WNCPPS GKSSPKNSIC AVRWA RK SLKTKKIPTÉ

601 WASI*ITPAT LPATCFVIP RPKTSTAKSA *PVRANATVT TQEIKK*LRF

651 QALPELMPCL AGTIKMLTLP LPQPICSIKN IGVRTLCRVI RAAILPG*IT

701 VS

FIGURE 23B (suite)

1 ATGCAAATAC CATTTCATTT GGCTTTATTA CCCACGCTGA TTATTGCTTC

51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG

101 CCACGCTACC TACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC

151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT

201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA

251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC

301 ATCGACGCCG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGCGCGGCTT

351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC

401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT

451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GCGGGCGGTG TCATCAACAT

501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT

551 ATGGTTCGTG GG AACCGT AGCTGAATA TGGAC CAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTCGGACTG CTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

1151 TTTCCGCCTC CATCAACCC TACGACCGCG CAAGCTGGCC GCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAA ACTCTA TCTGCGCGGT

1751 TCGTTGGGCG TGATGCAGGC GAAAGTCGTT GAAGACAAAG AAAATCCCGA

1801 CCGAGTGGGC ATCCATTTGA ATAACACCAG CAACGTTACC GGCAACCTGT

1851 TTTTCCGTTA TACCCCGACC GAAAACCTCT ACGGCGAAAT CGGCGTAACC

1901 GGTACAGGCA AACGCTACGG TTACGACTCA AGAAATAAAG AAGTGACTAC

1951 GCTTCCAGGC TTGCCCCGAG TTGATGCCAT GCTTGGCTGG AACCATAAAA

2001 ATGTTAACGT TACCTTTGCC GCAGCCAATC TGTTCAATCA AAAATATTGG

2051 CGTTCGGACT CTATGCCGGG TAATCCGCGC GGCTATACTG CCCGGGTAAA

2101 TTACCGTTTC TGA

FIGURE 24A (suite 3)

FIGURE 24B

1 MQIPFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNLTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTL

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

551 NPYYAVSGK H GVELSA IGQIPKKTLL SARFVG G ESR*RQRKSR

601 PSGHPFE*HQ QRYRQPVFPL YPDRKPLRRN RRNRYRQTLR LRLKK*RSY

651 ASRLCPS*CH AWLEP*KC*R YLCRSQSVQS KILAFGLYAG *SARLYCPGK

701 LPFL

FIGURE 24B (suite)

FIGURE 25A

1 ATGAAAATAT CATTTCAATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCTG CCTACGATAT GCGCGGCGAA AGCATTTTCC TCGCGGTTT
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC
451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGGCGGCG TCATCAACAT
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGTGCGGTTT

551 ACGGTTCTGT GGC ACCGC AGCCTGAATA TGGACATTAA CGAAGTGTTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTGGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGCTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA TTTCACGCTA

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCATTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC CTTAGGTTAC AGCCGCGCCT

1151 T TACTGCTTC CATCGATC TACGACCGAG CAAGCTGGCC CTTCGGGC

1201 AGATTGCAGC CTATCCTCAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCCGATTTG AAATTCGTCC

1301 TCGGCGGTCTG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAATAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CAACACGTCTG

1501 TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGTGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA CGAGCAAAAT

1651 GATCCCTACA CTTGGGCAGT CGGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC

1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT

1851 TTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GCGGTAACCG

1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG

1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA

2001 TGTTAACATT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC

2051 GTTCGGATGC CATGCCCGGC GCGCCGCGCA CTTATACGGC GCGGGTTAAT

2101 TACAGTTTCT AA

FIGURE 25A (suite 3)

FIGURE 25B

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLLSNFTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGY SRAFTASIDP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSINTS

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDEQN

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DRAW

551 DPYTWAVGGK HRSWELSA IGQIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNI TFAAANLLNQ KYWRSDAMPG APRTYTARVN

701 YSF*

FIGURE 25B (suite)

1 ATGAAAATAT CATTTCAATT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCTG CCTACGATAT GCGCGGTGAA AGCATTTTCC TGCGCGGTTT
351 TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC
401 AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAT CCTGAAAGGC
451 CCGTCTTCCG TGCTTTACGG CCGCACCAAC GCGGGCGGCG TCATCAACAT
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGAGCGGTTT

551 ACGGCTCATG GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG

601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC

651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA

701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC

751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG

801 CTTCGGACTG CTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA

851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC

901 AAATGGCGTG CCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT

951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC

1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC

1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT

1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT

1151 TTTCCGCCTC CATCAACCTACGACCGCG CAAGCTGGCCCTTCGGGC

1201 AGATTGCAGC CTATTCTGAC CCAAACCGC CACAAAGCCG ACTCCTACGG

1251 CATCTTTGTG CAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC

1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC

1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC

1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG

1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG

1501 TCTTCCGCCG TGTTC AACGC CGACCCCGAG TACACCCGCC AATACGAAAC

1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG

1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGA TCCAAAAAAC

1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC

1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT

1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGC GTAACCG

1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG

1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA

2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC

2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT

2101 TACCGTTTCT GA

FIGURE 26A (suite 3)

FIGURE 26B

1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL

51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG

101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG

151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL

201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD

251 NVERTPDRSP TKSVDYDRFGL PYRMGFAHRN DFKDKLQVW RSDLEYAFND

301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSNLTL

351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG

401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLGGRYDK YTFNSENKLT

451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGAFAPYGG RGGYLSIDTL

501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN

13-07-1999

EP99401764.8

DRAW

551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGSLGVMQA KVVEDKENPD

601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT

651 LPGFARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN

701 YRF*

FIGURE 26B (suite)

1 MKRFTYTLSD GLCIEIELKR SAKKNLILRP VNMQTVSINV PPFFQDHALA

51 NWLAANETIL RNTLAKMPVH PVSHPNLPEW IWYRGIKTKL DTHSQSHIRI

101 TSSEILLPRK ETAAQIDHLR RLLNERAREY LLPRLEKHAA ETGLTPAATD

151 LSNAKTFWGV CRPHTGIRLN WRLIGTPEYV ADYVCIELC HLRHPDHSPR

201 FWHLVNTLTP HTDNAKSWLK AHGRELFVLG *

FIGURE 27B

1 ATGAAACGCT TCACCTATAC TCTTTCCGAC GGCTTGTGCA TCGAAATCGA

51 ACTCAAACGC AGTGCCAAGA AAAATCTGAT TCTGCGCCCC GTCAATATGC

101 AGACGGTCAG CATCAACGTC CCACCCTTTT TTCAAGACCA CGCGTTAGCA

151 AACTGGCTGG CGGCAAACGA AACGATTTTG CGGAACACGC TTGCTAAAAT

201 GCCCGTGCAT CCTGTTTCCC ACCCAAACCTT ACCCGAGTGG ATTTGGTATC

251 GGGGAATAAA GACCAAGCTG GATACCCACA GCCAAAGCCA TATCCGTATC

301 ACGTCGTCTG AAATCCTGCT TCCCCGAAAA GAAACCGCCG CACAAATCGA

351 CCACCTGCGC CGCCTGTTGA ACGAACGCGC CCGCGAATAC CTGCTGCCCC

401 GCCTTGAAAA ACACGCAGCC GAAACAGGAC TGA CTCCCGC TGCCACAGAC

451 CTGAGCAACG CCAAAACCTT TTGGGGCGTA TGCCGCCCCG ACACCGGCAT

501 CCGCCTCAAC TGGCGGCTGA TCGGCACGCC CGAATACGTC GCCGACTATG

551 TCTGCA⁺TCCA CGAACTCT⁺ CACCTCCGCC ACCCCGACCA C⁺GTCCGCGC

601 TTTTGGCATT TGGTGAACAC GCTGACGCCG CATACCGACA ATGCTAAAAG

651 TTGGCTGAAG GCGCACGGGC GGGAATTGTT TGTGCTGGGG TAA

FIGURE 27B (suite)

FIGURE 28A

1 ATGAGCAAGA TTATTGTGCT GACCGCAGGC CACAGCAACA CCGACCCGGG

51 TCGGGTCAAC GGAAGCGACC GTGAGGCGGA CTTGGCGCAG GATATGCGCA

101 ACATTGTGGC TTCAATCCTG CGTAACGATT ACGGCCTGAC CGTTAAAACC

151 GACGGCACGG GCAAAGGCAA TATGCCGCTG CGCGAAGCGG TCAAGCTGAT

201 TCGCGGCTCG GATGTGGCGA TTGAGTTTCA CACCAACGCT GCCGTCAGCA

251 AAGCGGCGAC AGGCATCGAA GCCTTGAGTA CCGTTAAAAA CAAACGCTGG

301 TGTCAGGTGT TGAGCAAAGC CGTTGCCAAG AAAACCGGCT GGAAACTGCG

351 CGGCGAAGAC GGCTTTAAAC CCGACAATGC GGGCCAGCAT TCGCGCCTGG

401 CTTATGCACA AGCCGGCGGC ATTGTGTTTG AGCCTTTTTT CATCAGCAAC

451 GACACTGATT TGGCCTTGTT TAAGACGACT AAATGGGGCA TCTGCCGCGC

501 GATTGCGGAC GCGATTGCGA TGGAATTGGG GCGGCAAGA GTATGA

1 MSKIIVLTAG HSNTDPGAVN GSDREADLAQ DMRNIVASIL RNDYGLTVKT

51 DGTGKGNMPL REAVKLIRGS DVAIEFHTNA AVSKAATGIE ALSTVKNKRW

101 CQVLSKAVAK KTGWKLARGED GFKPDNAGQH SRLAYAQAGG IVFEPFFISN

151 DTDLALFKTT KWGICRAIAD AIAMELGAAR V*

FIGURE 29A

1 ATGCGTATTT TGGATATTTT TAAAAACCCA GCGACAGGCA ATGTGTCGCA

51 CTCGAAACTG TGGGCAAACG TTGCCTGCGC GCGGGGACG GTTAAGTTTG

101 TGATGCTGCC CGACCCGTCG GCGGAGATTT GGGCGGTGTA TTTGGGCATT

151 GTCGGCGGCT ATGCGGTGGC GCGTTCGTTG GTCAGCGTCA AACGTCAGGA

201 GGTCGAGAAT GAATCTCGTG AACTGCTGG CGAATAA

1 MRILDIFKNP ATGNVSHSKL WANVACAAGT VKFVMLPDPS AEIWAVYLG

51 VGGYAVARSL VSVKRQEVEN ESRETAGE*

FIGURE 30A

1 ATGCGGTGGC GCGTTCGTTG GTCAGCGTCA AACGTCAGGA GGTCGAGAAT

51 GAATCTCGTG AAAGTGCTGG CGAATAACTG GCAACCGATT GCCATCATCG

101 CGCTTGTCGG CACGGGTTTG GCGGTGTCGC ACCATCAAGG CTACAAGTCG

151 GCTTTTGCGA AGCAGCAGGC GGTCATTGAG AAAATGAAGC GCGACAAGGC

201 GCAAGCCCTG CTGTTGTCGG CTCAAAACTA CGCCCGCGAA CTGGAACAGG

251 CGCGTGCGGA AGCTAAAAAA TATGAAGTCA AGGCGCACGC CGTCGGCATG

301 GCTTTGGCGA AAAAACAGGC GGAAGTCAGC CGTCTGAAAA CGGAAAATAA

351 AAAGGAAATC GAAAATGTCC TTAAGTCAAGA CCGTAAAAAT GCAGGCGGCG

401 GTTGTATTGA CGGCTTTGGC CATCACGGCT TGCAGCTCTA CAAGCGCGCC

451 CTCGGCTACG GAAATTAA

1 MRWRVRWSAS NVRRSRMNLV KLLANNWQPI AIIALVGTGL AVSHHQGYKS

51 AFAKQQAVIE KMKRDKAQAL LLSAQNYARE LEQARAEAKK YEVKAHAVGM

101 ALAKKQAEVS RLKTENKKEI ENVLTQDRKN AGGGCIDGFG HHGLQLYKRA

151 LGYGN*

FIGURE 31A

1 ATGTCCTTAC TCAAGACCGT AAAAATGCAG GCGGCGGTTG TATTGACGGC

51 TTTGGCCATC ACGGCTTGCA GCTCTACAAG CGCGCCCTCG GCTACGGAAA

101 TTAAGGTTGT CGAAAAGGCG GTCATGCCGA CACCGCCTGC CGCGTTGATG

151 GTCGCGCCGG TCGCCCCGAA TCCGCCGAAA GACGGCAAGA CGGCCACGCT

201 GTTGGAACAC GCCGCCGAGT TTGGCGGCTA TGTTGCCGAA CTTGAAAACC

251 AAAATCAGGC TTGGCGCGAC TGGGCGGGCA ATCACTCCCG CAAAGTCGGA

301 AACTGA

1 MSLLKTVKMQ AAVVLTALAI TACSSTSAPS ATEIKVVEKA VMPTPPAALM

51 VAPVRPNPPK DGKTATLLEH AAEEGGYVAE LENQNQAWRD WAGNHSRKVG

101 N*

1 GTGCTGGCAG TTTTGCTTGC TGGTGTAGCC TTCGCCCTGA GCGATGATTT
51 CATGGTTGGC TGCTTTCAAA CGCCAACGGT ATTCGCCTTT TCGGTCTTTA
101 TAGATTTCAA AATACATAAG GTTTCTCCTA TGAATGAGTA CACGTTTTCT
151 TACCGCTTTA ACGGCAAGTC CTGGTCATTG AGCATTGTTGG CGGACAACCC
201 TGAAGAAGCC AGGGCGAAAT TTCGGGCTGC ACGAGAAAAT GCGCACTATG
251 ACGGCGAAGT TGTAGCAAAG GTTTATACAT TTGTAAATAT TTCGTGGGTT
301 AAGAAATTGT ACAAGCGGAC AAAATATTTA ATGGGTATCA AAGAATGA

FIGURE 32B

1 VLAVLLAGVA FALSDDFMVG CFQTPTVFAF CVFIDFKIHK VSPMNEYTFS

51 YRFNGKSWSL SIWADNPEEA RAKFRAAREN AHYDGEVVAK VYTFVNISWV

101 KKLYKRTKYL MGIKE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAAGAGGC TTATGCCCG CAGGTAAAGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 33A (suite 2)

1 MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 34A (suite 2)

1 MTLNLMMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT ATGCAAGATT ACGGTATTTT CGTTTGCCTG

51 AACTGACGC CCTATTTGCA ACATGAACTA TTTTCGGCTA TGAAATCCTA

101 TTTTCCAAA TATATCCTAC CCGTTTCACT TTTTACCTTG CCACTATCCC

151 TTTCCCATC CGTTTCGGCT TTTACGCTGC CTGAAGCATG GCGGGCGGCG

201 CAGCAACATT CGGCTGATTT TCAAGCGTCC CATTACCAGC GTGATGCAGT

251 GCGCGCACGG CAACAACAAG CCAAGGCCGC ATTCCTTCCC CATGTATCCG

301 CCAATGCCAG CTACCAGCGC CAGCCGCCAT CGATTTCTTC CACCCGCGAA

351 ACACAGGGAT GGAGCGTGCA GGTGGGACAA ACCTTATTTG ACTCTGCCAA

401 ATTTGCACAA TACCGCCAAA GCAGGTTCTGA TACGCAGGCT GCAGAACAGC

451 GTTTCGATGC GGCACGCGAA GAATTGCTGT TGAAAGTTGC CGAAAGTTAT

501 TTCAACGTTT TACTCAGCCG AGACACCGTT GCCGCCCATG CGGCGGAAAA

551 AGAGGCTTAT GCCCAGCAGG TAAGGCAGGC GCAGGCTTTA TTCAATAAAG

601 GTGCTGCCAC CGCGCTAGAT ATTCACGAAG CCAAAGCCGG TTACGACAAT

651 GCCCTGGCCC AAGAAATCGC CGTATTGGCT GAGAAACAAA CCTATGAAAA

701 CCAGTTGAAC GACTACACCG GCCTGGACAG CAAACAAATC GAGGCCATAG

751 ATACCGCCAA CCTGTTGGCA CGCTATCTGC CCAAGCTGGA ACGTTACAGT

801 CTGGATGAAT GGCAGCGCAT TGCCTTATCC AACAATCATG AATACCGGAT

851 GCAGCAGCTT GCCCTGCAAA GCAGCGGACA GGCCTTCGG GCAGCACAGA

901 ACAGCCGCTA TCCCACCGTT TCTGCCCATG TCGGCTATCA GAATAACCTC

951 TACACTTCAT CTGCGCAGAA TAATGACTAC CACTATCGGG GCAAAGGGAT

1001 GAGCGTCGGC GTACAGTTGA ATTTGCCGCT TTATACCGGC GGAGAATTGT

1051 CGGGCAAAAT CCATGAAGCC GAAGCGCAAT ACGGGGCTGC CGAAGCACAG

1101 CTGACCGCAA CCGAGCGGCA CATCAAATC GCCGTACGCC AGGCTTATAC

1151 CGAAAGCGGT GCGGCGCGTT ACCAAATCAT GCGCAAGAA CGGGTTTTGG

1201 AAAGCAGCCG TTTGAAACTG AAATCGACCG AAACCGGCCA ACAATACGGC

1251 ATCCGCAACC GGCTGGAAGT AATACGGGCG CGGCAGGAAG TCGCCCAAGC

1301 AGAACAGAAA CTGGCTCAAG CACGGTATAA ATTCATGCTG GCTTATTTGC

1351 GCTTGGTGAA AGAGAGCGGG TTAGGGTTGG AAACGGTATT TCGGGAATAA

FIGURE 35A (suite 2)

1 MTLLNLICKI TVFPFA*H*R PICNMNYFRL *NPIFPNISY PFHFLPCHYP

51 FPHPFRLLRC LKHGGRRSNI RLIFKRPITS VMQCAHGNNK PRPHSFPMYP

101 PMPATSASRH RFLPPAKHRD GACRWDKPYL TLPNLHNTAK AGSIRRLQNS

151 VSMRHAKNCC *KLPKVISTF YSAETPLPPM RRKKRLMPSR *GRRRLYSIK

201 VLPPR*IFTK PKPVTTMPWP KKSPYWLRNK PMKTS*TTTP AWTANKSRP*

251 IPPTCWAHAIC PSWNVTVWMN GSALPYPTIM NTGCSSLPCK AADRRFGQHR

301 TAAIPPFLPM SAIRITSTLH LRRIMTTTIG AKG*ASAYS* ICRFIPAENC

351 RAKSMKPKRN TGLPKHS*PQ PSGTSNSPYA RLIPKAVRRV TKS WRKNGFW

401 KAAV*N*NRP KPANNTASAT GWK*YGRGRK SPKQNRNWLK HGINSCWLIC

451 AW*KRAG*GW KRYLRN

FIGURE 36A

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGGGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG

401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAGAGGC TTATGCCAG CAGGTAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 36A (suite 2)

1 MTLNLNMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CGAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAAGAGGC TTATGCCAC CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTAACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

1151 ATACCGAAAG CCGGCGGCG CGTTACCAA TCATGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 37A (suite 2)

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG

401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAAGAGGC TTATGCCAG CAGGTAAGC AGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 38A (suite 2)

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAGAGGG TTATGCCAG CAGTGGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAAGCTT

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCGAG GAAGTCGCCC

1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 39A (suite 2)

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GCGCAGCAA CATTGGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAGAGGG TTATGCCAG CAGGAGGG AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTAACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

1151 ATACCGAAAG CCGCGGCG CGTTACCAA TCATCGCA AGAACGGGT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 40A (suite 2)

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG

401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 41A (suite 1)

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 41A (suite 2)

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAAGAGGC TTATGCCCGAG CAGGTATGCC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTAACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 42A (suite 1)

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 42A (suite 2)

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGGCTG ATTTTCAAGC GTCCATTAC CAGCGTGATG
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301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
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501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAAAGAGGC TTATGCCCGAG CAGGTAAAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 43A (suite 2)

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
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401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
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651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTAACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

FIGURE 44A (suite 1)

FIGURE 44B

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA

251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA

301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE

351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV

401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*

1151 ATACCGAAAG CGGTGCG CGTTACCAA TCATGGCGCA AACGGGT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 44B (suite)

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG

51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTTCG GCTATGAAAT

101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA

151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC

201 GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG

251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA

301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG

351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG

401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA

451 CAGCGTTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG

501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG

551 AAAGAGGC TTATGCCAG CAAGAGGC AGGCGCAGGC TTTATTCAAT

601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA

651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG

701 AAAACCAAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC

751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA

801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC

851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA

901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA

951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG

1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA

1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC

1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT

1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT

1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA

1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCAG GAAGTCGCCC

1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1401 ATAA

FIGURE 45A (suite 2)

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL

51 SLSPSVSAFT LPEAWRAAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV

101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE

151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN

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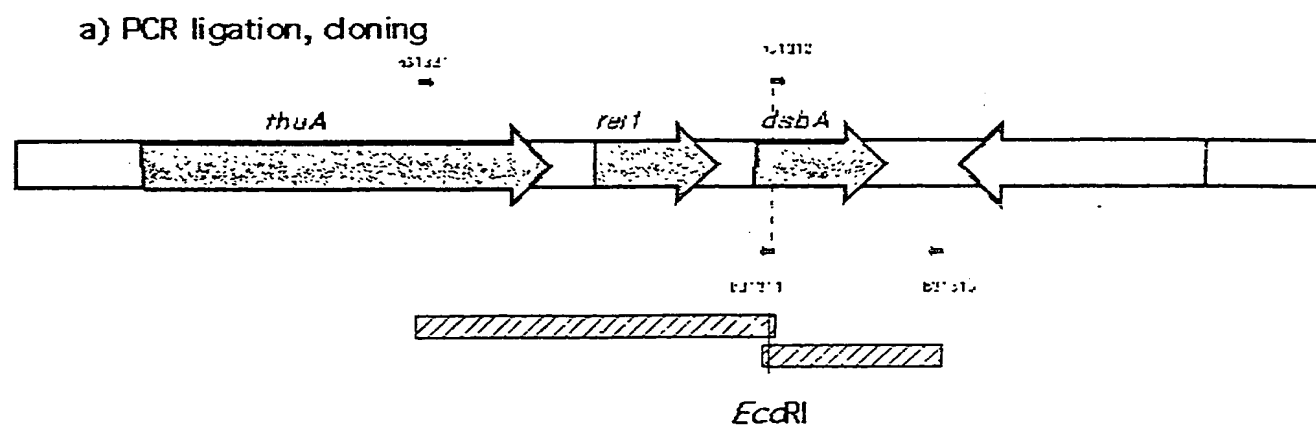
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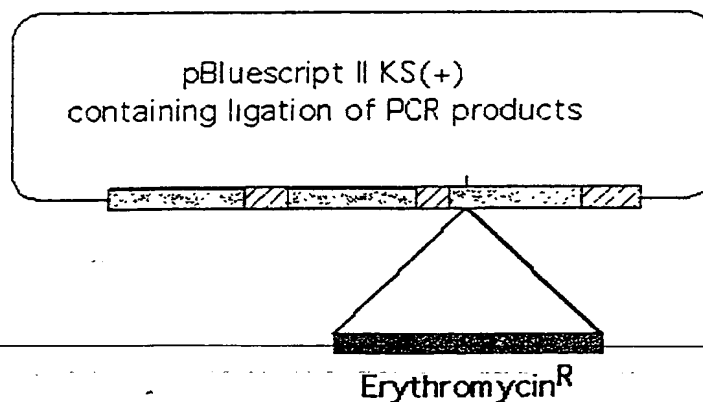
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401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY

451 LRLVKESGLG LETVFAE*



b) Insertion of erythromycin resistance cassette



c) Transformation of *Nm* to erythromycin resistance and DsbA1⁻

FIGURE 46



FIGURE 47A

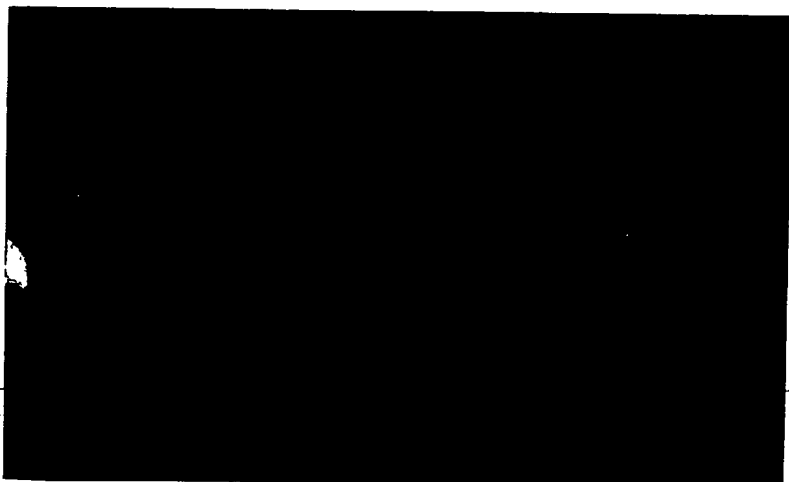


FIGURE 47B

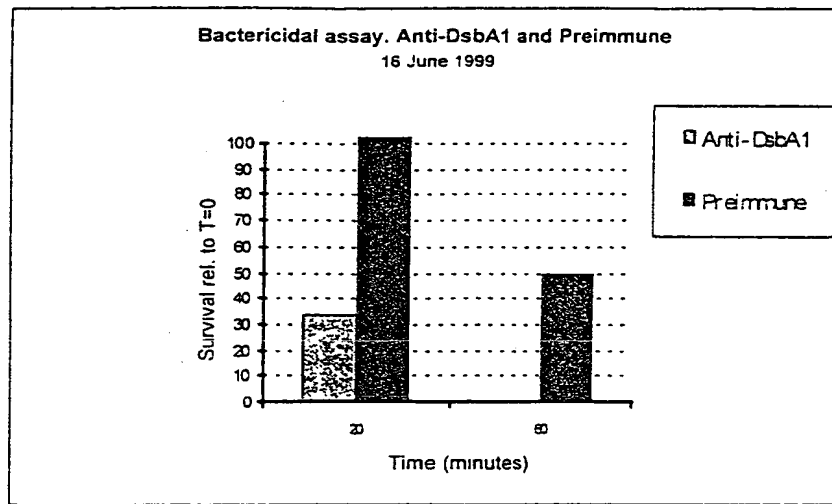


FIGURE 48

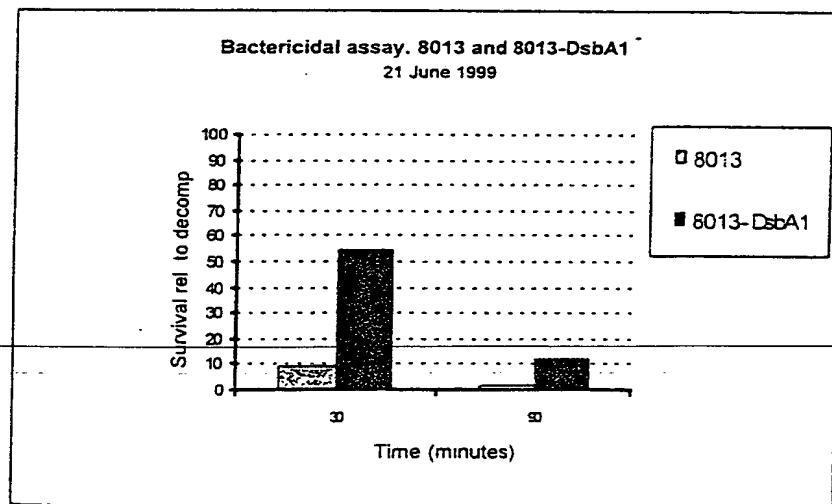


FIGURE 49

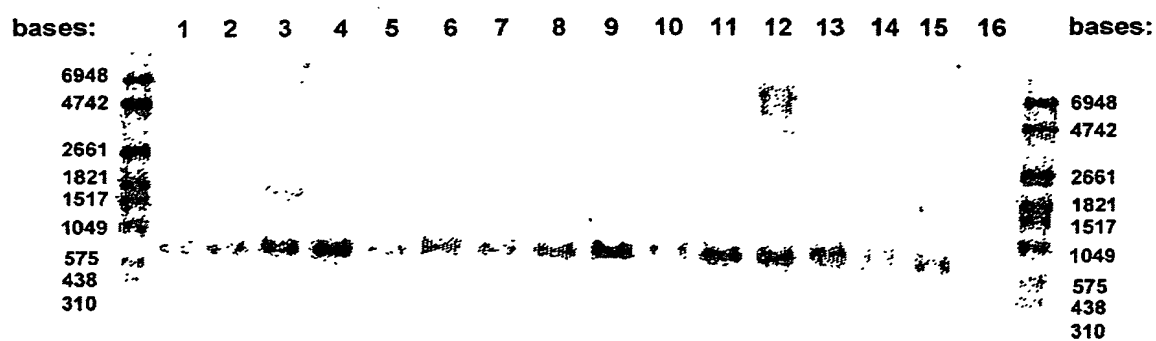


FIGURE 50

" "

SEQUENCE LISTING

<110> I. N. S. E. R. M.

MAX-PLANCK-GESELLSCHAFT ZUR FORDERUNG DES WISSENSC

<120> Novel *Neisseria meningitidis* compounds and
anti-infection applications thereof

<130> 989 SEQUENCES

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His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
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Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
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Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
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Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
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Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
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Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
 180 185 190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
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Glu Glu Gln Lys Lys Pro Gln
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gacggcaaaa aagtattggc tgcatttgag gtccttgaaa gccaaagcgcg tgcggctcaa 540
atggaagagt tgaccaataa attccaaatc agcggcacac cgactgtgat tgcggcggc 600
aaataccaag ttgaatttaa agactggcag tccggtatga ccacgattga ccagttggtg 660
gataaagtac gcgaagagca gaaaaagccg caataa 696

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<210> 4

<211> 231

<212> PRT

<213> Neisseria meningitidis

<400> 4

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Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
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Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Ala
      20              25              30

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Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Glu Leu Asn Glu Gly
    35              40              45

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```

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
    50              55              60

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Lys Ile Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
    65              70              75              80

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```

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
      85              90              95

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Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
100              105              110

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Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
    115              120              125

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```

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
    130              135              140

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Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
    145              150              155              160

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Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala

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165

170

175

Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
 180 185 190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
 195 200 205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
 210 215 220

Glu Glu Gln Lys Lys Pro Gln
 225 230

<210> 5

<211> 696

<212> DNA

<213> Neisseria meningitidis

<400> 5

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 gcccctgctg agttgaacga aggtgtgaac tacactgtat tgtctacgcc tattccgcaa 180
 cagcaggccg gtaaaatcga agtattggaa tttttcggct acttctgccc gcattgcgcc 240
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 cgggagcatg tcgtgtgggg tgatgaaatg aaacctttgg caggtttggc ggccgcagtg 360
 gaaatggccg gtgaatcaga taaagccaac agccatattt tcgatgcgat ggtaaatcaa 420
 aaaatcaatc tggccgatac cgataccctg aaaaaatggc tgtccgagca aacagcgttt 480
 gacggcaaaa aagtattggc tgcatttgag gctcctgaaa gccaaagcgc tgccggctcaa 540
 atggaagagt tgaccaataa attccaaatc agcggcacac cgactgtgat tgccggcggc 600
 aaataccaag ttgaatttaa agactggcag tccggtatga ccacgattga ccagttgggt 660
 gataaagtac gcgaagagca gaaaaagccg caataa 696

<210> 6

<211> 231

<212> PRT

<213> Neisseria meningitidis

<400> 6

Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
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Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Ala
 20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Glu Leu Asn Glu Gly
 35 40 45

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Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
   50                      55                      60

Lys Ile Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
   65                      70                      75                      80

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
                      85                      90                      95

Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
   100                      105                      110

Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
   115                      120                      125

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
   130                      135                      140

Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
   145                      150                      155                      160

Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
                      165                      170                      175

Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
                      180                      185                      190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
   195                      200                      205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
   210                      215                      220

Glu Glu Gln Lys Lys Pro Gln
   225                      230

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<210> 7

<211> 696

<212> DNA

<213> Neisseria meningitidis

<400> 7

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gccctgctg agttgaacga aggtgtgaac tacactgtat tgtctacgcc tattccgcaa 180
cagcaggccg gtaaaatcga agtattggaa tttttcggct acttctgccc gcattgcgcc 240

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catcttgagc cggctcttgag cgagcacatc aaaacgttta aagacgatac ctatatgcg 300
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gaaatggccg gtgaatcaga taaagccaac agccatattt tcgatgcat gggttaatcaa 420
aaaatcaatc tggccgatac cgataccctg aaaaaatggc tgtccgagca aacagcgttt 480
gacggcaaaa aagtattggc tgcatttgag gctcctgaaa gccaaagcgcg tgcggctcaa 540
atggaagagt tgaccaataa attccaaatc agcggcacac cgactgtgat tgcggcggcg 600
aaataccaag ttgaatttaa agactggcag tccggtatga ccacgattga ccagttgggtg 660
gataaagtac gcgaagagca gaaaaagccg caataa 696

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<210> 8

<211> 231

<212> PRT

<213> Neisseria meningitidis

<400> 8

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Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
  1              5              10              15

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Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Ala
          20              25              30

```

```

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Glu Leu Asn Glu Gly
      35              40              45

```

```

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
      50              55              60

```

```

Lys Ile Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
      65              70              75              80

```

```

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
          85              90              95

```

```

Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
      100              105              110

```

```

Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
      115              120              125

```

```

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
      130              135              140

```

```

Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
      145              150              155              160

```

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Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
      165              170              175

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Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
 180 185 190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
 195 200 205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
 210 215 220

Glu Glu Gln Lys Lys Pro Gln
 225 230

<210> 9
 <211> 696
 <212> DNA
 <213> Neisseria meningitidis

<400> 9
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 gccctgctg agttgaacga aggtgtgaac tacactgtat tgtctacgcc tattccgcaa 180
 cagcaggccg gtaaaatcga agtattggaa tttttcggct acttctgccc gcattgcgcc 240
 catcttgagc cggctctgag cgagcacatc aaaacgttta aagacgatac ctatatgcgc 300
 cgggagcatg tcgtgtggg tgatgaaatg aaacctttgg cacgtttggc ggccgcagtg 360
 gaaatggccg gtgaatcaga taaagccaac agccatattt tcgatgcatg ggtaaatcaa 420
 aaaatcaatc tggccgatac cgataccctg aaaaaatggc tgtccgagca aacagcgttt 480
 gacggcaaaa aagtattggc tgcatttgag gctcctgaaa gccaaagcgcg tgcggctcaa 540
 atggaagagt tgaccaataa attccaaatc agcggcacac cgactgtgat tgcggcggc 600
 aaataccaag ttgaatttaa agactggcag tccggtatga ccacgattga ccagttgggtg 660
 gataaagtac gcgaagagca gaaaaagccg caataa 696

<210> 10
 <211> 231
 <212> PRT
 <213> Neisseria meningitidis

<400> 10
 Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
 1 5 10 15

Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Ala
 20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Glu Leu Asn Glu Gly
 35 40 45

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly

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      50              55              60
Lys Ile Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
 65              70              75              80

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
      85              90              95

Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
      100              105              110

Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
      115              120              125

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
      130              135              140

Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
      145              150              155              160

Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
      165              170              175

Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
      180              185              190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
      195              200              205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
      210              215              220

Glu Glu Gln Lys Lys Pro Gln
      225              230

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<210> 11
<211> 696
<212> DNA
<213> Neisseria meningitidis

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<400> 11
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gccctgctg agttgaacga aggtgtgaac tacactgtat tgtctacgcc tattccgcaa 180
cagcaggccg gtaaaatcga agtattggaa tttttcggct acttctgccc gcattgcgcc 240
catcttgagc cggctcttgag cgagcacatc aaaacgttta aagacgatac ctatatgcgc 300
cgggagcatg tcgtgtgggg tgatgaaatg aaacctttgg cacttttggc ggccgcagtg 360

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gaaatggccg gtgaatcaga taaagccaac agccatattt tcgatgcat ggттаатcaa 420
 aaaatcaatc tggccgatac cgataccctg aaaaaatggc tgtccgagca aacagcgttt 480
 gacggcaaaa aagtattggc tgcatttgag gctcctgaaa gccaaagcgcg tgcggctcaa 540
 atggaagagt tgaccaataa attccaaatc agcggcacac cgactgtgat tgcggcggc 600
 aaataccaag ttgaatttaa agactggcag tccggtatga ccacgattga ccagttggtg 660
 gataaagtac gcgaagagca gaaaaagccg caataa 696

<210> 12

<211> 231

<212> PRT

<213> Neisseria meningitidis

<400> 12

Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
 1 5 10 15

Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Ala
 20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Glu Leu Asn Glu Gly
 35 40 45

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
 50 55 60

Lys Ile Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
 65 70 75 80

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
 85 90 95

Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
 100 105 110

Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
 115 120 125

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
 130 135 140

Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
 145 150 155 160

Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
 165 170 175

Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
 180 185 190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
 195 200 205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
 210 215 220

Glu Glu Gln Lys Lys Pro Gln
 225 230

<210> 13

<211> 696

<212> DNA

<213> Neisseria meningitidis

<400> 13

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 cagcaggccg gtaaaatcga agtattggaa tttttcggct acttctgccc gcattgcgcc 240
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 cgggagcatg tcgtgtgggg tgatgaaatg aaacctttgg cacgtttggc ggccgcagtg 360
 gaaatggccg gtgaatcaga taaagccaac agccatattt tcgatgcatg ggtaaatcaa 420
 aaaatcaatc tggccgatac cgataccctg aaaaaatggc tgtccgagca aacagcgttt 480
 gacggcaaaa aagtattggc tgcatttgag gctcctgaaa gccaaagcgc tgccggctcaa 540
 atggaagagt tgaccaataa attccaaatc agcggcacac cgactgtgat tgcggcggc 600
 aaataccaag ttgaatttaa agactggcag tccggtatga ccacgattga ccagttggtg 660
 gataaagtac gcgaagagca gaaaaagccg caataa 696

<210> 14

<211> 231

<212> PRT

<213> Neisseria meningitidis

<400> 14

Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
 1 5 10 15

Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Ala
 20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Glu Leu Asn Glu Gly
 35 40 45

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
 50 55 60

Lys Ile Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
65 70 75 80

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
85 90 95

Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
100 105 110

Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
115 120 125

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
130 135 140

Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
145 150 155 160

Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
165 170 175

Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
180 185 190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
195 200 205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
210 215 220

Glu Glu Gln Lys Lys Pro Gln
225 230

<210> 15

<211> 696

<212> DNA

<213> Neisseria meningitidis

<400> 15

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cagcaggccg gtaaaatcga agtattggaa tttttcggct acttctgccc gcattgcgcc 240
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cgggagcatg tcgtgtgggg tgatgaaatg aaacctttgg cacttttggc ggccgcagtg 360
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gacggcaaaa aagtattggc tgcatttgag gctcctgaaa gccaaagcgcg tgcggctcaa 540
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 aaataccaag ttgaatttaa agactggcag tccggtatga ccacgattga ccagttggtg 660
 gataaagtac gcgaagagca gaaaaagccg caataa 696

<210> 16

<211> 231

<212> PRT

<213> Neisseria meningitidis

<400> 16

Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
 1 5 10 15

Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Ala
 20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Glu Leu Asn Glu Gly
 35 40 45

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
 50 55 60

Lys Ile Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
 65 70 75 80

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
 85 90 95

Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
 100 105 110

Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
 115 120 125

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
 130 135 140

Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
 145 150 155 160

Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
 165 170 175

Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
 180 185 190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp

195

200

205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
 210 215 220

Glu Glu Gln Lys Lys Pro Gln
 225 230

<210> 17

<211> 696

<212> DNA

<213> Neisseria meningitidis

<400> 17

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 gaaatggccg gtgaatcaga taaagccaac agccatattt tcgatgcgat ggtaaatcaa 420
 aaaatcaatc tggccgatac cgataccctg aaaaaatggc tgtccgagca aacagcgttt 480
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 aaataccaag ttgaatttaa agactggcag tctggtatga ccacgattga ccagttggtg 660
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<210> 18

<211> 231

<212> PRT

<213> Neisseria meningitidis

<400> 18

Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
 1 5 10 15

Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Ala
 20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Glu Leu Asn Glu Gly
 35 40 45

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Ala Gly
 50 55 60

Lys Ile Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
 65 70 75 80

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
 85 90 95
 Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
 100 105 110
 Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
 115 120 125
 Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
 130 135 140
 Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
 145 150 155 160
 Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
 165 170 175
 Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
 180 185 190
 Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
 195 200 205
 Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
 210 215 220
 Glu Glu Gln Lys Lys Pro Gln
 225 230

<210> 19

<211> 696

<212> DNA

<213> Neisseria meningitidis

<400> 19

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 aaacaggctg aaaccagtgt tccggcagac agcgcccaaa gcagctcatc tgctccggca 120
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 cagcaggccg gtaaaatcga agtattggaa tttttcggct acttctgccc gcattgcgcc 240
 catcttgagc cggctcttgag cgagcacatc aaaacgttta aagacgatac ctatatgcgc 300
 cgggagcatg tcgtgtgggg tgatgaaatg aaacctttgg cacgtttggc ggccgcagtg 360
 gaaatggccg gtgaatcaga taaagccaac agccatattt tcgatgcgat ggtaaatcaa 420
 aaaatcaatc tggccgatac cgataccctg aaaaaatggc tgtccgagca aacagcgttt 480
 gacggcaaaa aagtattggc tgcatttgag gctcctgaaa gccaaagcgcg tgcggctcaa 540
 atggaagagt tgaccaataa attccaaatc agcggcacac cgactgtgat tgcggcggc 600

aaataccaag ttgaatttaa agactggcag tctggtatga ccacgattga ccagttggtg 660
 gataaagtac gcgaagagca gaaaaagccg caataa 696

<210> 20

<211> 231

<212> PRT

<213> Neisseria meningitidis

<400> 20

Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
 1 5 10 15

Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Ala
 20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Glu Leu Asn Glu Gly
 35 40 45

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
 50 55 60

Lys Ile Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
 65 70 75 80

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
 85 90 95

Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
 100 105 110

Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
 115 120 125

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
 130 135 140

Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
 145 150 155 160

Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
 165 170 175

Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
 180 185 190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
 195 200 205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
 210 215 220

Glu Glu Gln Lys Lys Pro Gln
 225 230

<210> 21
 <211> 696
 <212> DNA
 <213> Neisseria meningitidis

<400> 21
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 gccccagccc cattgaccga aggcgtgaac tacactgtat tgtccacgcc tatcccgcaa 180
 cagcaggccg gcaaagtcga agtcttggaa tttttcggct acttctgccc gcattgcgcc 240
 catcttgagc cggctcttgag cgagcacatc aaaacgttta aagacgatac ctatatgcgc 300
 cgggagcatg tcgtgtgggg tgatgaaatg aaacctttgg cacgtttggc ggccgcagtg 360
 gaaatggccg gtgaatcaga taaagccaac agccatattt tcgatgcatg ggttaatcaa 420
 aaaatcaatc tggccgatac cgataccctg aaaaaatggc tgtccgagca aacagcgttt 480
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 atggaagagt tgaccaataa attccaaatc agcggcacac cgactgtgat cgtcggcggc 600
 aaataccaag ttgaatttaa agactggcag tccggtatga ccacgattga ccagttggtg 660
 gataaagtac gcgaagagca gaaaaagccg caataa 696

<210> 22
 <211> 231
 <212> PRT
 <213> Neisseria meningitidis

<400> 22
 Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
 1 5 10 15

Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Val
 20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Pro Leu Thr Glu Gly
 35 40 45

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
 50 55 60

Lys Val Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
 65 70 75 80

His	Leu	Glu	Pro	Val	Leu	Ser	Glu	His	Ile	Lys	Thr	Phe	Lys	Asp	Asp		
85						90						95					
Thr	Tyr	Met	Arg	Arg	Glu	His	Val	Val	Trp	Gly	Asp	Glu	Met	Lys	Pro		
100						105						110					
Leu	Ala	Arg	Leu	Ala	Ala	Ala	Val	Glu	Met	Ala	Gly	Glu	Ser	Asp	Lys		
115						120						125					
Ala	Asn	Ser	His	Ile	Phe	Asp	Ala	Met	Val	Asn	Gln	Lys	Ile	Asn	Leu		
130						135						140					
Ala	Asp	Thr	Asp	Thr	Leu	Lys	Lys	Trp	Leu	Ser	Glu	Gln	Thr	Ala	Phe		
145						150						155				160	
Asp	Gly	Lys	Lys	Val	Leu	Ala	Ala	Phe	Glu	Ala	Ser	Glu	Ser	Gln	Ala		
165						170						175					
Arg	Ala	Ala	Gln	Met	Glu	Glu	Leu	Thr	Asn	Lys	Phe	Gln	Ile	Ser	Gly		
180						185						190					
Thr	Pro	Thr	Val	Ile	Val	Gly	Gly	Lys	Tyr	Gln	Val	Glu	Phe	Lys	Asp		
195						200						205					
Trp	Gln	Ser	Gly	Met	Thr	Thr	Ile	Asp	Gln	Leu	Val	Asp	Lys	Val	Arg		
210						215						220					
Glu	Glu	Gln	Lys	Lys	Pro	Gln											
225						230											

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<210> 23
<211> 696
<212> DNA
<213> Neisseria meningitidis
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<400> 23							
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gccccagccc	cattgaccga	aggcgtgaac	tacactgtat	tgtccacgcc	tatcccgcaa		180
cagcaggccg	gcaaagtcga	agtcttgga	tttttcggct	acttctgccc	gcattgcgcc		240
catcttgagc	cggctcttgag	cgagcacatc	aaaacgttta	aagacgatac	ctatatgcgc		300
cgggagcatg	tcgtgtgggg	tgatgaaatg	aaacctttgg	cacgtttggc	ggccgcagtg		360
gaaatggccg	gtgaatcaga	taaagccaac	agccatattt	tcgatgcgat	ggttaatcaa		420
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gacggcaaaa	aagtattggc	tgcatttgag	gcttctgaaa	gccaagcgcg	tgcggtcaa		540
atggaagagt	tgaccaataa	attccaaatc	agcggcacac	cgactgtgat	cgtcggcggc		600
aaataccaag	ttgaatttaa	agactggcag	tccggtatga	ccacgattga	ccagttggtg		660

gataaagtac gcgaagagca gaaaaagccg caataa

696

<210> 24

<211> 231

<212> PRT

<213> Neisseria meningitidis

<400> 24

Met Lys Leu Lys Thr Leu Ala Leu Thr Ser Leu Thr Leu Leu Ala Leu
1 5 10 15

Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Val
20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Pro Leu Thr Glu Gly
35 40 45

Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
50 55 60

Lys Val Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
65 70 75 80

His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
85 90 95

Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
100 105 110

Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
115 120 125

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
130 135 140

Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
145 150 155 160

Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Ser Glu Ser Gln Ala
165 170 175

Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
180 185 190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
195 200 205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg

210

220

Glu Glu Gln Lys Lys Pro Gln
225 230

<210> 25
<211> 696
<212> DNA
<213> Neisseria meningitidis

<400> 25
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gccccagccc cattgaccga aggcgtgaac tacactgtat tgtccacgcc tatcccgcaa 180
cagcaggccg gcaaagtcga agtcttgga tttttcggct acttctgccc gcattgcgcc 240
catcttgagc cggctcttgag cgagcacatc aaaacgttta aagacgatac ctatatgcgc 300
cgggagcatg tcgtgtgggg tgatgaaatg aaacctttgg cacgtttggc ggccgcagtg 360
gaaatggccg gtgaatcaga taaagccaac agccatattt tcgatgcgat ggtaaatcaa 420
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gacggcaaaa aagtattggc tgcatttgag gctcctgaaa gccaagcgcg tgcggctcaa 540
atggaagagt tgaccaataa attccaaatc agcggcacac cgactgtgat tgcggcgggc 600
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gataaagtac gcgaagagca gaaaaagccg caataa 696

<210> 26
<211> 231
<212> PRT
<213> Neisseria meningitidis

<400> 26
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Ala Ala Cys Ser Lys Gln Ala Glu Thr Ser Val Pro Ala Asp Ser Val
20 25 30

Gln Ser Ser Ser Ser Ala Pro Ala Ala Pro Ala Pro Leu Thr Glu Gly
35 40 45
Val Asn Tyr Thr Val Leu Ser Thr Pro Ile Pro Gln Gln Gln Ala Gly
50 55 60
Lys Val Glu Val Leu Glu Phe Phe Gly Tyr Phe Cys Pro His Cys Ala
65 70 75 80
His Leu Glu Pro Val Leu Ser Glu His Ile Lys Thr Phe Lys Asp Asp
85 90 95

Thr Tyr Met Arg Arg Glu His Val Val Trp Gly Asp Glu Met Lys Pro
 100 105 110

Leu Ala Arg Leu Ala Ala Ala Val Glu Met Ala Gly Glu Ser Asp Lys
 115 120 125

Ala Asn Ser His Ile Phe Asp Ala Met Val Asn Gln Lys Ile Asn Leu
 130 135 140

Ala Asp Thr Asp Thr Leu Lys Lys Trp Leu Ser Glu Gln Thr Ala Phe
 145 150 155 160

Asp Gly Lys Lys Val Leu Ala Ala Phe Glu Ala Pro Glu Ser Gln Ala
 165 170 175

Arg Ala Ala Gln Met Glu Glu Leu Thr Asn Lys Phe Gln Ile Ser Gly
 180 185 190

Thr Pro Thr Val Ile Val Gly Gly Lys Tyr Gln Val Glu Phe Lys Asp
 195 200 205

Trp Gln Ser Gly Met Thr Thr Ile Asp Gln Leu Val Asp Lys Val Arg
 210 215 220

Glu Glu Gln Lys Lys Pro Gln
 225 230

<210> 27

<211> 1047

<212> DNA

<213> Neisseria meningitidis

<400> 27

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 cgatattcta atcaattgct tgaccgatat caaaaaaatc caagtagttt aaataatcaa 180
 gaaaaaaata ttcttgcata ttttattaac caaacctctg gaggtaacac agcttgggca 240
 gcttcgatac tgaaaacgcc ccagtcaatg ggtaatctca ctattccttc caagatatatt 300
 aataacacct tatcgaaagc ctatcaaaca ttgagtcgtt atgattcttt tgattacaaa 360
 tcagctgttg ccgcacaacc tgcactttac ttattaaacg gaccgcttgg cttcagtgtc 420
 aaagcagcta ctgtggcagc aggaggatat aacattggac agggagcgaa agcaatctct 480
 aatggagaat atctgcatgg tacagttcag gttgttaatg gcacattgat ggttgcagga 540
 tctgtatctg cacaggctgc aatatcggcc aagcctgcac ctgttaccgg ttatctgagc 600
 aatgacagtg ctctgtcttt aagacaagct ttaactgctg aaagccagag aatccgcatg 660
 aaactgccgg aagagtatcg acaaataagg aatcttgcca tagcaaaaat tgatgttaaa 720
 ggattaccgc aaaggatgga agcatttagt tctttccaaa aaggggaaca tggatttatt 780

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tcgttacctg aaacaaaaat ttttaaacct atatctgttg ataaatatca taatattgcc 840
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gcacagcaac tcggaaataa tcgtaatgta tcaggtagaa ttgatctatt tacagaatta 960
aaggcctgtc aatcttgcag caatgttatt ttagagttta gaaatcgcta tccaaatatt 1020
caattaaata tttttacagg aaaatag                                     1047

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<210> 28

<211> 348

<212> PRT

<213> Neisseria meningitidis

<400> 28

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Glu Tyr Ala Leu Arg Glu Lys Leu Ile Lys Lys Ala Lys Gly Lys Gly
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Leu Leu Ser Leu Asp Trp Gly Ser Leu Thr Glu Gln Glu Ala Arg Gln
      20             25             30

```

```

Phe Ile Tyr Leu Ile Glu Lys Asp Arg Tyr Ser Asn Gln Leu Leu Asp
      35             40             45

```

```

Arg Tyr Gln Lys Asn Pro Ser Ser Leu Asn Asn Gln Glu Lys Asn Ile
      50             55             60

```

```

Leu Ala Tyr Phe Ile Asn Gln Thr Ser Gly Gly Asn Thr Ala Trp Ala
      65             70             75             80

```

```

Ala Ser Ile Leu Lys Thr Pro Gln Ser Met Gly Asn Leu Thr Ile Pro
      85             90             95

```

```

Ser Lys Asp Ile Asn Asn Thr Leu Ser Lys Ala Tyr Gln Thr Leu Ser
      100            105            110

```

```

Arg Tyr Asp Ser Phe Asp Tyr Lys Ser Ala Val Ala Ala Gln Pro Ala
      115            120            125

```

```

Leu Tyr Leu Leu Asn Gly Pro Leu Gly Phe Ser Val Lys Ala Ala Thr
      130            135            140

```

```

Val Ala Ala Gly Gly Tyr Asn Ile Gly Gln Gly Ala Lys Ala Ile Ser
      145            150            155            160

```

```

Asn Gly Glu Tyr Leu His Gly Thr Val Gln Val Val Asn Gly Thr Leu
      165            170            175

```

```

Met Val Ala Gly Ser Val Ser Ala Gln Ala Ala Ile Ser Ala Lys Pro
      180            185            190

```

Ala Pro Val Thr Arg Tyr Leu Ser Asn Asp Ser Ala Pro Ala Leu Arg
195 200 205

Gln Ala Leu Thr Ala Glu Ser Gln Arg Ile Arg Met Lys Leu Pro Glu
210 215 220

Glu Tyr Arg Gln Ile Gly Asn Leu Ala Ile Ala Lys Ile Asp Val Lys
225 230 235 240

Gly Leu Pro Gln Arg Met Glu Ala Phe Ser Ser Phe Gln Lys Gly Glu
245 250 255

His Gly Phe Ile Ser Leu Pro Glu Thr Lys Ile Phe Lys Pro Ile Ser
260 265 270

Val Asp Lys Tyr His Asn Ile Ala Ser Pro Pro Arg Gly Thr Leu Arg
275 280 285

Asn Ile Asp Gly Glu Tyr Lys Leu Leu Glu Thr Ile Ala Gln Gln Leu
290 295 300

Gly Asn Asn Arg Asn Val Ser Gly Arg Ile Asp Leu Phe Thr Glu Leu
305 310 315 320

Lys Ala Cys Gln Ser Cys Ser Asn Val Ile Leu Glu Phe Arg Asn Arg
325 330 335

Tyr Pro Asn Ile Gln Leu Asn Ile Phe Thr Gly Lys
340 345

<210> 29

<211> 2112

<212> DNA

<213> Neisseria meningitidis

<400> 29

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gtggtcggac agtccgacac cagcgctactc aaaggctaca tcaactacga cgaagccgcc 180
gttaccgcga acggacagct catcaaagaa acgccgcaaa ccatcgatac gctcaatatc 240
cagaaaaaca aaaattacgg cacgaacgat ttgagttcca tcctcgaagg caatgccggc 300
atcgacgccg cctacgatat gcgcggcgaa agcattttcc tgcgcggcgtt tcaagccgac 360
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ggtacggttt atggttcgtg ggcaaaccgc agcctgaata tggacatcaa cgaagtgtg 600
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 accaagtccg tgtacgaccg cttcggactg ccttaccgca tgggggttcgc ccaccggaac 840
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<210> 30

<211> 703

<212> PRT

<213> Neisseria meningitidis

<400> 30

Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
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Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr
 20 25 30

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
 35 40 45

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
 50 55 60

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
 65 70 75 80

Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu

85	90	95
Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile 100	105	110
Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly 115	120	125
Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg 130	135	140
Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn 145	150	155 160
Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln 165	170	175
Ser Arg Asn Ile Gly Thr Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu 180	185	190
Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu 195	200	205
Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser 210	215	220
Lys Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly 225	230	235 240
Leu Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro 245	250	255
Asp Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr 260	265	270
Arg Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln 275	280	285
Val Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala 290	295	300
Gln Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe 305	310	315 320
Tyr Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp 325	330	335
Gln Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Leu Thr Leu Asn Gly		

340	345	350
Asp Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp		
355	360	365
Tyr Ser Arg Glu His Arg Asn Pro Thr Leu Gly Phe Ser Ser Ala Phe		
370	375	380
Ser Ala Ser Ile Asn Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly		
385	390	395
Arg Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr		
405	410	415
Gly Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe		
420	425	430
Val Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys		
435	440	445
Leu Thr Gly Ser Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn		
450	455	460
Ile Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser		
465	470	475
Tyr Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser		
485	490	495
Ile Asp Thr Leu Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr		
500	505	510
Arg Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu		
515	520	525
Ser Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr		
530	535	540
Arg Pro Asp Pro Lys Asn Asn Pro Tyr Ile Tyr Ala Val Ser Gly Lys		
545	550	555
His Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro		
565	570	575
Lys Lys Leu Tyr Leu Arg Gly Ser Leu Gly Val Met Gln Ala Lys Val		
580	585	590
Val Glu Asp Lys Glu Asn Pro Asp Arg Val Gly Ile His Leu Asn Asn		

595

600

605

Thr Ser Asn Val Thr Gly Asn Leu Phe Phe Arg Tyr Thr Pro Thr Glu
610 615 620

Asn Leu Tyr Gly Glu Ile Gly Val Thr Gly Thr Gly Lys Arg Tyr Gly
625 630 635 640

Tyr Asp Ser Arg Asn Lys Glu Val Thr Thr Leu Pro Gly Phe Ala Arg
645 650 655

Val Asp Ala Met Leu Gly Trp Asn His Lys Asn Val Asn Val Thr Phe
660 665 670

Ala Ala Ala Asn Leu Phe Asn Gln Lys Tyr Trp Arg Ser Asp Ser Met
675 680 685

Pro Gly Asn Pro Arg Gly Tyr Thr Ala Arg Val Asn Tyr Arg Phe
690 695 700

<210> 31

<211> 2113

<212> DNA

<213> Neisseria meningitidis

<400> 31

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caaaacatct tctccgccac gatttg aaattcggtcc tcggcggtccg tggacaaa 1320
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gcttggtctg aaccataaaa atgttaacgt tacctttgcc gcagccaatc tgttcaatca 2040
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ttaccgtttc tga 2113

```

<210> 32

<211> 697

<212> PRT

<213> Neisseria meningitidis

<400> 32

```

Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
  1             5             10             15

```

```

Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr
      20             25             30

```

```

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
      35             40             45

```

```

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
      50             55             60

```

```

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
      65             70             75             80

```

```

Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu
      85             90             95

```

```

Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile
      100            105            110

```

```

Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly
      115            120            125

```

```

Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg
      130            135            140

```

Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn
145 150 155 160

Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln
165 170 175

Ser Arg Asn Ile Gly Thr Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu
180 185 190

Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu
195 200 205

Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser
210 215 220

Lys Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly
225 230 235 240

Leu Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro
245 250 255

Asp Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr
260 265 270

Arg Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln
275 280 285

Val Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala
290 295 300

Gln Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe
305 310 315 320

Tyr Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp
325 330 335

Gln Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Leu Thr Leu Asn Gly
340 345 350

Asp Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp
355 360 365

Tyr Ser Arg Glu His Arg Asn Pro Thr Leu Gly Phe Ser Ser Ala Phe
370 375 380

Ser Ala Ser Ile Asn Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly
385 390 395 400

Arg Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr
 405 410 415

Gly Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe
 420 425 430

Val Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys
 435 440 445

Leu Thr Gly Ser Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn
 450 455 460

Ile Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser
 465 470 475 480

Tyr Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser
 485 490 495

Ile Asp Thr Leu Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr
 500 505 510

Arg Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu
 515 520 525

Ser Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr
 530 535 540

Arg Pro Asp Pro Lys Asn Asn Pro Tyr Ile Tyr Ala Val Ser Gly Lys
 545 550 555 560

His Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro
 565 570 575

Lys Lys Thr Leu Ser Ala Arg Phe Val Gly Arg Asp Ala Gly Glu Ser
 580 585 590

Arg Arg Gln Arg Lys Ser Arg Pro Ser Gly His Pro Phe Glu His Gln
 595 600 605

Gln Arg Tyr Arg Gln Pro Val Phe Pro Leu Tyr Pro Asp Arg Lys Pro
 610 615 620

Leu Arg Arg Asn Arg Arg Asn Arg Tyr Arg Gln Thr Leu Arg Leu Arg
 625 630 635 640

Leu Lys Lys Arg Ser Asp Tyr Ala Ser Arg Leu Cys Pro Ser Cys His
 645 650 655

Ala Trp Leu Glu Pro Lys Cys Arg Tyr Leu Cys Arg Ser Gln Ser Val
660 665 670

Gln Ser Lys Ile Leu Ala Phe Gly Leu Tyr Ala Gly Ser Ala Arg Leu
675 680 685

Tyr Cys Pro Gly Lys Leu Pro Phe Leu
690 695

<210> 33

<211> 2111

<212> DNA

<213> *Neisseria meningitidis*

<400> 33

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gtggtcggac agtccgacac cagcgtactc aaaggtaca tcaactacga cgaagccgcc 180
gttaccgcga acggacagct catcaaagaa acgccgcaaa ccatcgatac gctcaatata 240
cagaaaaaca aaaattacgg tacgaacgat ttgagttcca tctcgaagg caatgccggc 300
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```

```

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ttggctggaa ccataaaaaat gttaacgtta cctttgccgc agccaatctg ttcaatcaaa 2040
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```

<210> 34

<211> 700

<212> PRT

<213> Neisseria meningitidis

<400> 34

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Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
  1             5             10             15

```

```

Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr
      20             25             30

```

```

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
      35             40             45

```

```

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
      50             55             60

```

```

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
      65             70             75             80

```

```

Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu
      85             90             95

```

```

Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile
      100            105            110

```

```

Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly
      115            120            125

```

```

Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg
      130            135            140

```

```

Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn
      145            150            155            160

```

```

Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln
      165            170            175

```

```

Ser Arg Asn Ile Gly Ala Val Tyr Gly Ser Arg Ala Asn Arg Ser Leu
      180            185            190

```

Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu
 195 200 205

Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser
 210 215 220

Lys Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly
 225 230 235 240

Leu Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro
 245 250 255

Asp Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr
 260 265 270

Arg Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln
 275 280 285

Val Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala
 290 295 300

Gln Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe
 305 310 315 320

Tyr Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp
 325 330 335

Gln Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Phe Thr Leu Asn Gly
 340 345 350

Asp Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp
 355 360 365

Tyr Ser Arg Glu His Arg Asn Pro Thr Leu Gly Tyr Ser Arg Ala Phe
 370 375 380

Thr Ala Ser Ile Asp Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly
 385 390 395 400

Arg Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr
 405 410 415

Gly Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe
 420 425 430

Val Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys
 435 440 445

Leu Thr Gly Ser Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn
450 455 460

Ile Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser
465 470 475 480

Tyr Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser
485 490 495

Ile Asp Thr Ser Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr
500 505 510

Arg Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asn Arg Leu
515 520 525

Asp Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr
530 535 540

Arg Pro Asp Ala Glu Asn Asn Pro Tyr Thr Trp Ala Val Gly Gly Lys
545 550 555 560

His Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro
565 570 575

Lys Lys Leu Tyr Leu Arg Gly Ser Leu Gly Val Met Gln Ala Lys Val
580 585 590

Val Glu Asp Lys Lys Asn Pro Asp Arg Val Gly Ile His Leu Asn Asn
595 600 605

Thr Ser Asn Val Thr Gly Asn Leu Phe Phe Arg Tyr Thr Arg Pro Lys
610 615 620

Thr Ser Thr Ala Lys Ser Ala Pro Val Gln Ala Asn Ala Thr Val Thr
625 630 635 640

Thr Gln Glu Ile Lys Lys Leu Arg Phe Gln Ala Leu Pro Glu Leu Met
645 650 655

Pro Cys Leu Ala Gly Thr Ile Lys Met Leu Thr Leu Pro Leu Pro Gln
660 665 670

Pro Ile Cys Ser Ile Lys Asn Ile Gly Val Arg Thr Leu Cys Arg Val
675 680 685

Ile Arg Ala Ala Ile Leu Pro Gly Ile Thr Val Ser
690 695 700

<210> 35

<211> 2112

<212> DNA

<213> *Neisseria meningitidis*

<400> 35

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gtggtcggac agtccgacac cagcgtactc aaaggctaca tcaactacga cgaagccgcc 180
gttaccgcga acggacagct catcaaagaa acgccgcaaa ccatcgatac gctcaatata 240
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cttggttgga accataaaaa tggttaacatt acctttgccg cagccaatct gctcaatcaa 2040
aatattggc gttcggatgc catgcccggc gcgccgcgca cttatacggc gcgggttaat 2100
tacagtttct aa 2112

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<210> 36

<211> 703

<212> PRT

<213> *Neisseria meningitidis*

<400> 36

Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
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Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr
 20 25 30

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
 35 40 45

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
 50 55 60

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
 65 70 75 80

Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu
 85 90 95

Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile
 100 105 110

Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly
 115 120 125

Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg
 130 135 140

Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn
 145 150 155 160

Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln
 165 170 175

Ser Arg Asn Ile Gly Ala Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu
 180 185 190

Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu
 195 200 205

Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser
 210 215 220

Lys Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly
 225 230 235 240

Leu Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro

245	250	255
Asp Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr		
260	265	270
Arg Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln		
275	280	285
Val Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala		
290	295	300
Gln Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe		
305	310	315
Tyr Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp		
325	330	335
Gln Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Leu Thr Leu Asn Gly		
340	345	350
Asp Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp		
355	360	365
Tyr Ser Arg Glu His Arg Asn Pro Thr Leu Gly Phe Ser Ser Ala Phe		
370	375	380
Ser Ala Ser Ile Asn Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly		
385	390	395
Arg Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ala Tyr		
405	410	415
Gly Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe		
420	425	430
Val Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys		
435	440	445
Leu Thr Gly Ser Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn		
450	455	460
Ile Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser		
465	470	475
Tyr Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser		
485	490	495
Ile Asn Thr Ser Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr		

500

505

510

Arg Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu
515 520 525

Ser Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr
530 535 540

Arg Pro Asp Glu Gln Asn Asp Pro Tyr Thr Trp Ala Val Gly Gly Lys
545 550 555 560

His Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro
565 570 575

Lys Lys Leu Tyr Leu Arg Gly Ser Leu Gly Val Met Gln Ala Lys Val
580 585 590

Val Glu Asp Lys Glu Asn Pro Asp Arg Val Gly Ile His Leu Asn Asn
595 600 605

Thr Ser Asn Val Thr Gly Asn Leu Phe Phe Arg Tyr Thr Pro Thr Glu
610 615 620

Asn Leu Tyr Gly Glu Ile Gly Val Thr Gly Thr Gly Lys Arg Tyr Gly
625 630 635 640

Tyr Asn Ser Arg Asn Lys Glu Val Thr Thr Leu Pro Gly Phe Ala Arg
645 650 655

Val Asp Ala Met Leu Gly Trp Asn His Lys Asn Val Asn Ile Thr Phe
660 665 670

Ala Ala Ala Asn Leu Leu Asn Gln Lys Tyr Trp Arg Ser Asp Ala Met
675 680 685

Pro Gly Ala Pro Arg Thr Tyr Thr Ala Arg Val Asn Tyr Ser Phe
690 695 700

<210> 37

<211> 2112

<212> DNA

<213> Neisseria meningitidis

<400> 37

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gtggtcggac agtccgacac cagcgtactc aaaggctaca tcaactacga cgaagccgcc 180

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```

<210> 38

<211> 702

<212> PRT

<213> *Neisseria meningitidis*

<400> 38

Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala

1

5

10

15

Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr

20

25

30

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser

35

40

45

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
50 55 60

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
65 70 75 80

Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu Gly
85 90 95

Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile Phe
100 105 110

Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly Val
115 120 125

Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg Val
130 135 140

Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn Gly
145 150 155 160

Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln Ser
165 170 175

Arg Asn Ile Gly Ala Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu Asn
180 185 190

Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu Thr
195 200 205

Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser Lys
210 215 220

Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly Leu
225 230 235 240

Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro Asp
245 250 255

Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr Arg
260 265 270

Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln Val
275 280 285

Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala Gln
290 295 300

Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe Tyr
305 310 315 320

Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp Gln
325 330 335

Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Phe Thr Leu Asn Gly Asp
340 345 350

Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp Tyr
355 360 365

Ser Arg Glu His Arg Asn Pro Thr Leu Gly Tyr Ser Arg Ala Phe Thr
370 375 380

Ala Ser Ile Asp Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly Arg
385 390 395 400

Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr Gly
405 410 415

Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe Val
420 425 430

Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys Leu
435 440 445

Thr Gly Ser Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn Ile
450 455 460

Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser Tyr
465 470 475 480

Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser Ile
485 490 495

Asn Thr Ser Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr Arg
500 505 510

Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu Ser
515 520 525

Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr Arg
530 535 540

Pro Asp Glu Gln Asn Asp Pro Tyr Thr Trp Ala Val Gly Gly Lys His
545 550 555 560

Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro Lys
565 570 575

Lys Leu Tyr Leu Arg Gly Ser Leu Gly Val Met Gln Ala Lys Val Val
580 585 590

Glu Asp Lys Glu Asn Pro Asp Arg Val Gly Ile His Leu Asn Asn Thr
595 600 605

Ser Asn Val Thr Gly Asn Leu Phe Phe Arg Tyr Thr Pro Thr Glu Asn
610 615 620

Leu Tyr Gly Glu Ile Gly Val Thr Gly Thr Gly Lys Arg Tyr Gly Tyr
625 630 635 640

Asn Ser Arg Asn Lys Glu Val Thr Thr Leu Pro Gly Phe Ala Arg Val
645 650 655

Asp Ala Met Leu Gly Trp Asn His Lys Asn Val Asn Ile Thr Phe Ala
660 665 670

Ala Ala Asn Leu Leu Asn Gln Lys Tyr Trp Arg Ser Asp Ala Met Pro
675 680 685

Gly Ala Pro Arg Thr Tyr Thr Ala Arg Val Asn Tyr Ser Phe
690 695 700

<210> 39

<211> 2112

<212> DNA

<213> Neisseria meningitidis

<400> 39

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gttaccgcga acggacagct catcaaagaa acgccgcaaa ccatcgatac gctcaatatc 240
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aacaaaaacg tcgccatccg tctcaccggc gaagtcgggc gcgccaattc gttccgcagc 660
ggcatagaca gcaaaaatgt catggtttcg cccagcatta ccgtcaaact cgacaacggc 720
ttgaagtga cggggcaata cacctacgac aatgtggagc gcacgccga ccgcagtcgc 780

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cttggctgga accataaaaa tgttaacgtt acctttgccg cagccaatct gttcaatcaa 2040
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taccgtttct ga 2112

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<210> 40

<211> 702

<212> PRT

<213> Neisseria meningitidis

<400> 40

Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala

1

5

10

15

Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr

20

25

30

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser

35

40

45

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn

50

55

60

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile

65

70

75

80

Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu Gly

85

90

95


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Asn Ala Gly Ile Asp Ala      Tyr Asp Met Arg Gly Glu Ser  Phe
      100                      105                      110

Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly Val
      115                      120                      125

Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg Val
      130                      135                      140

Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn Gly
      145                      150                      155                      160

Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln Ser
      165                      170                      175

Arg Asn Ile Gly Ala Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu Asn
      180                      185                      190

Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu Thr
      195                      200                      205

Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser Lys
      210                      215                      220

Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly Leu
      225                      230                      235                      240

Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro Asp
      245                      250                      255

Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr Arg
      260                      265                      270

Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln Val
      275                      280                      285

Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala Gln
      290                      295                      300

Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe Tyr
      305                      310                      315                      320

Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp Gln
      325                      330                      335

Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Phe Thr Leu Asn Gly Asp
      340                      345                      350

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Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp Tyr
 355 360 365

Ser Arg Glu His Arg Asn Pro Thr Leu Gly Tyr Arg Gly Ser Phe Thr
 370 375 380

Val Pro Ile Asn Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly Arg
 385 390 395 400

Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr Gly
 405 410 415

Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe Val
 420 425 430

Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys Leu
 435 440 445

Thr Gly Asn Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn Ile
 450 455 460

Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser Tyr
 465 470 475 480

Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser Ile
 485 490 495

Asp Thr Leu Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr Arg
 500 505 510

Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu Ser
 515 520 525

Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr Arg
 530 535 540

Pro Asp Pro Lys Asn Asn Pro Tyr Ile Tyr Ala Val Ser Gly Lys His
 545 550 555 560

Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro Lys
 565 570 575

Lys Leu Tyr Leu Arg Gly Ser Leu Gly Val Met Gln Ala Lys Val Val
 580 585 590

Glu Asp Lys Glu Asn Pro Asp Arg Val Gly Ile His Leu Asn Asn Thr
 595 600 605

Ser Asn Val Thr Gly Asn Phe Phe Arg Tyr Thr Pro Thr Asn
 610 615 620
 Leu Tyr Gly Glu Ile Gly Val Thr Gly Thr Gly Lys Arg Tyr Gly Tyr
 625 630 635 640
 Asn Ser Arg Asn Lys Glu Val Thr Thr Leu Pro Gly Phe Ala Arg Val
 645 650 655
 Asp Ala Met Leu Gly Trp Asn His Lys Asn Val Asn Val Thr Phe Ala
 660 665 670
 Ala Ala Asn Leu Phe Asn Gln Lys Tyr Trp Arg Ser Asp Ser Met Pro
 675 680 685
 Gly Asn Pro Arg Gly Tyr Thr Ala Arg Val Asn Tyr Arg Phe
 690 695 700

<210> 41

<211> 2112

<212> DNA

<213> Neisseria meningitidis

<400> 41

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 gtggtcggac agtccgacac cagcgtactc aaaggctaca tcaactacga cgaagccgcc 180
 gttacccgca acggacagct catcaaagaa acgccgcaaa ccatcgatac gctcaatatc 240
 cagaaaaaca aaaattacgg tacgaacgat ttgagttcca tcctcgaagg caatgccggc 300
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 aacaaaaacg tcgccatccg tctcaccggc gaagtcgggc gcgccaattc gttccgcagc 660
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tacaccttta attccgaaaa caaactcacc ggcagcagcc gccaatagag cggacactcg 1380
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cttggttgga accataaaaa tggttaacgtt acctttgccg cagccaatct gttcaatcaa 2040
aaatattggc gttcggactc tatgccgggt aatccgcgcg gctatactgc ccgggtaaat 2100
taccgtttct ga 2112

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<210> 42

<211> 702

<212> PRT

<213> Neisseria meningitidis

<400> 42

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Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
  1             5             10             15

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Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr
      20             25             30

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Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
      35             40             45

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Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
      50             55             60

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Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
      65             70             75             80

```

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Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu
      85             90             95

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Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile
      100            105            110

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Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly
      115            120            125

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Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg
      130            135            140

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Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn
145 150 155 160

Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln
165 170 175

Ser Arg Asn Ile Gly Ala Val Tyr Gly Trp Ala Asn Arg Ser Leu Asn
180 185 190

Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu Thr
195 200 205

Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser Lys
210 215 220

Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly Leu
225 230 235 240

Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro Asp
245 250 255

Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr Arg
260 265 270

Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln Val
275 280 285

Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala Gln
290 295 300

Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe Tyr
305 310 315 320

Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp Gln
325 330 335

Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Phe Thr Leu Asn Gly Asp
340 345 350

Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp Tyr
355 360 365

Ser Arg Glu His Arg Asn Pro Thr Leu Gly Tyr Asn Arg Ala Phe Ser
370 375 380

Ala Ser Ile Asn Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly Arg
385 390 395 400

Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr Gly
405 410 415

Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe Val
420 425 430

Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys Leu
435 440 445

Thr Gly Ser Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn Ile
450 455 460

Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser Tyr
465 470 475 480

Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser Ile
485 490 495

Asp Thr Leu Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr Arg
500 505 510

Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu Ser
515 520 525

Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr Arg
530 535 540

Pro Asp Pro Lys Asn Asn Pro Tyr Ile Tyr Ala Val Ser Gly Lys His
545 550 555 560

Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro Lys
565 570 575

Lys Leu Tyr Leu Arg Gly Ser Leu Gly Val Met Gln Ala Lys Val Val
580 585 590

~~Glu Asp Lys Glu Asn Pro Asp Arg Val Gly Ile His Leu Asn Asn Thr~~
~~595 600 605~~

Ser Asn Val Thr Gly Asn Leu Phe Phe Arg Tyr Thr Pro Thr Glu Asn
610 615 620

Leu Tyr Gly Glu Ile Gly Val Thr Gly Thr Gly Lys Arg Tyr Gly Tyr
625 630 635 640

Asp Ser Arg Asn Lys Glu Val Thr Thr Leu Pro Gly Phe Ala Arg Val
645 650 655

Asp Ala Met Leu Gly Trp Asn His Lys Asn Val Asn Val Thr Phe Ala
660 665 670

Ala Ala Asn Leu Phe Asn Gln Lys Tyr Trp Arg Ser Asp Ser Met Pro
675 680 685

Gly Asn Pro Arg Gly Tyr Thr Ala Arg Val Asn Tyr Arg Phe
690 695 700

<210> 43

<211> 2109

<212> DNA

<213> Neisseria meningitidis

<400> 43

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aactcaagaa ataaagaagt gaccacgctt ccaggctttg cccgagttga tgccatgctc 1980
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 cgtttctga 2109

<210> 44

<211> 702

<212> PRT

<213> Neisseria meningitidis

<400> 44

Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
 1 5 10 15

Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr
 20 25 30

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
 35 40 45

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
 50 55 60

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
 65 70 75 80

Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu
 85 90 95

Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile
 100 105 110

Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly
 115 120 125

Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg
 130 135 140

Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn
 145 150 155 160

Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln
 165 170 175

Ser Arg Asn Ile Gly Ala Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu
 180 185 190

Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu

195 200 205
 Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser
 210 215 220
 Lys Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly
 225 230 235 240
 Leu Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro
 245 250 255
 Asp Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr
 260 265 270
 Arg Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln
 275 280 285
 Val Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala
 290 295 300
 Gln Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe
 305 310 315 320
 Tyr Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp
 325 330 335
 Gln Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Leu Thr Leu Asn Gly
 340 345 350
 Asp Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp
 355 360 365
 Tyr Ser Arg Glu His Arg Asn Pro Thr Leu Gly Tyr Arg Gly Ser Phe
 370 375 380
 Thr Val Pro Ile Asn Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly
 385 390 395 400
 Arg Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr
 405 410 415
 Gly Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe
 420 425 430
 Val Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys
 435 440 445
 Leu Thr Gly Asn Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn

450	455	460
Ile Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser		
465	470	475 480
Tyr Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Tyr Leu Ser Ile		
485	490	495
Asp Thr Ser Ser Ala Ala Val Phe Asn Ala Ala Pro Glu Tyr Thr Arg		
500	505	510
Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu Ser		
515	520	525
Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr Arg		
530	535	540
Pro Asp Pro Lys Asn Asn Pro Tyr Ile Tyr Ala Val Ser Gly Lys His		
545	550	555 560
Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro Lys		
565	570	575
Lys Leu Tyr Leu Arg Gly Ser Leu Gly Val Met Gln Ala Lys Val Val		
580	585	590
Glu Asp Lys Glu Asn Pro Asp Arg Val Gly Ile His Leu Asn Asn Thr		
595	600	605
Ser Asn Val Thr Gly Asn Leu Phe Phe Arg Tyr Thr Pro Thr Glu Asn		
610	615	620
Leu Tyr Gly Glu Ile Gly Val Thr Gly Thr Gly Lys Arg Tyr Gly Tyr		
625	630	635 640
Asn Ser Arg Asn Lys Glu Val Thr Thr Leu Pro Gly Phe Ala Arg Val		
645	650	655
Asp Ala Met Leu Gly Trp Asn His Lys Asn Val Asn Val Thr Phe Ala		
660	665	670
Ala Ala Asn Leu Leu Asn Gln Lys Tyr Trp Arg Ser Asp Ser Met Pro		
675	680	685
Gly Asn Pro Arg Gly Tyr Thr Ala Arg Val Asn Tyr Arg Phe		
690	695	700

<210> 45
 <211> 2108
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 45
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 ggcggcgccg tcatcaacat ggtcagcaaa tacgccaaact tcaaacaaag ccgcaacatc 540
 ggtgcggttt acggttcgtg ggcaaacgc agcctgaata tggacattaa cgaagtgtg 600
 aacaaaaacg tcgccatccg tctcaccggc gaagtcgggc gcgccaattc gttccgcagc 660
 ggcatagaca gcaaaaatgt catggtttcg cccagcatta ccgtcaaact cgacaacggc 720
 ttgaagtga cggggcaata cacctacgac aatgtggagc gcacgccga ccgcagtccg 780
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 agattgcagc ctattctgac ccaaaaccgc caaaaagccg actcctacgg catctttgtg 1260
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 gtttctga 2108

<210> 46
 <211> 697
 <212> PRT
 <213> *Neisseria meningitidis*

<400> 46

Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
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Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr
 20 25 30

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
 35 40 45

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
 50 55 60

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
 65 70 75 80

Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu
 85 90 95

Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile
 100 105 110

Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly
 115 120 125

Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg
 130 135 140

Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn
 145 150 155 160

Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln
 165 170 175

Ser Arg Asn Ile Gly Ala Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu
 180 185 190

Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu
 195 200 205

Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser
 210 215 220

Lys Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly
 225 230 235 240

Leu Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro
 245 250 255

Asp Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr
260 265 270

Arg Met Gly Phe Ala His Pro Asn Asp Phe Val Lys Asp Lys Leu Gln
275 280 285

Val Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala
290 295 300

Gln Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe
305 310 315 320

Tyr Ala Gly Ser Glu Asn Gly Ser Arg Ile Lys Arg Asn Tyr Ala Trp
325 330 335

Gln Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Phe Thr Leu Asn Gly
340 345 350

Asp Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp
355 360 365

Tyr Ser Arg Glu His Arg Asn Pro Thr Leu Gly Tyr Arg Gly Ser Phe
370 375 380

Thr Val Pro Ile Asn Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly
385 390 395 400

Arg Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr
405 410 415

Gly Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe
420 425 430

Val Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys
435 440 445

Leu Thr Gly Asn Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn
450 455 460

Ile Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser
465 470 475 480

Tyr Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Tyr Leu Ser Ile
485 490 495

Asp Thr Ser Ser Ala Ala Val Phe Asn Ala Ala Pro Glu Tyr Thr Pro
500 505 510

Asn Thr Lys Pro Ala Ser Lys Ala Val Gly Trp Thr Ile Val Trp Thr
 515 520 525

Pro Pro Cys Arg Phe Thr Lys Ser Asn Ala Ser Ile Ser Ala Thr Ala
 530 535 540

Pro Ile Gln Lys Thr Thr Leu Ile Phe Met Arg Leu Ala Ala Asn Thr
 545 550 555 560

Val Arg Ala Ala Trp Asn Cys Pro Pro Ser Gly Lys Ser Ser Pro Lys
 565 570 575

Asn Ser Ile Cys Ala Val Arg Trp Ala Cys Arg Arg Lys Ser Leu Lys
 580 585 590

Thr Lys Lys Ile Pro Thr Glu Trp Ala Ser Ile Ile Thr Pro Ala Thr
 595 600 605

Leu Pro Ala Thr Cys Phe Ser Val Ile Pro Arg Pro Lys Thr Ser Thr
 610 615 620

Ala Lys Ser Ala Pro Val Arg Ala Asn Ala Thr Val Thr Thr Gln Glu
 625 630 635 640

Ile Lys Lys Leu Arg Phe Gln Ala Leu Pro Glu Leu Met Pro Cys Leu
 645 650 655

Ala Gly Thr Ile Lys Met Leu Thr Leu Pro Leu Pro Gln Pro Ile Cys
 660 665 670

Ser Ile Lys Asn Ile Gly Val Arg Thr Leu Cys Arg Val Ile Arg Ala
 675 680 685

Ala Ile Leu Pro Gly Ile Thr Val Ser
 690 695

<210> 47

<211> 2113

<212> DNA

<213> Neisseria meningitidis

<400> 47

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 gtggtcggac agtccgacac cagcgtactc aaaggctaca tcaactacga cgaagccgcc 180
 gttacccgca acggacagct catcaaagaa acgccgcaaa ccatcgatac gctcaatatc 240

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<210> 48

<211> 697

<212> PRT

<213> *Neisseria meningitidis*

<400> 48

Met Gln Ile Pro Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
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Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr
20 25 30

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
35 40 45

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
50 55 60

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
65 70 75 80

Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu
85 90 95

Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile
100 105 110

Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly
115 120 125

Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg
130 135 140

Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn
145 150 155 160

Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln
165 170 175

Ser Arg Asn Ile Gly Thr Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu
180 185 190

Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu
195 200 205

Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser
210 215 220

Lys Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly
225 230 235 240

Leu Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro
245 250 255

Asp Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr
260 265 270

Arg Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln
275 280 285

Val Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala
290 295 300

Gln Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe
305 310 315 320

Tyr Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp
325 330 335

Gln Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Leu Thr Leu Asn Gly
340 345 350

Asp Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp
355 360 365

Tyr Ser Arg Glu His Arg Asn Pro Thr Leu Gly Phe Ser Ser Ala Phe
370 375 380

Ser Ala Ser Ile Asn Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly
385 390 395 400

Arg Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr
405 410 415

Gly Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe
420 425 430

Val Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys
435 440 445

Leu Thr Gly Ser Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn
450 455 460

Ile Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser
465 470 475 480

Tyr Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser
485 490 495

Ile Asp Thr Leu Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr
500 505 510

Arg Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu
515 520 525

Ser Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr
530 535 540

Arg Pro Asp Pro Lys Asn Asn Pro Tyr Ile Tyr Ala Val Ser Gly Lys
545 550 555 560

His Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro
565 570 575

Lys Lys Thr Leu Ser Ala Arg Phe Val Gly Arg Asp Ala Gly Glu Ser
580 585 590

Arg Arg Gln Arg Lys Ser Arg Pro Ser Gly His Pro Phe Glu His Gln
595 600 605

Gln Arg Tyr Arg Gln Pro Val Phe Pro Leu Tyr Pro Asp Arg Lys Pro
610 615 620

Leu Arg Arg Asn Arg Arg Asn Arg Tyr Arg Gln Thr Leu Arg Leu Arg
625 630 635 640

Leu Lys Lys Arg Ser Asp Tyr Ala Ser Arg Leu Cys Pro Ser Cys His
645 650 655

Ala Trp Leu Glu Pro Lys Cys Arg Tyr Leu Cys Arg Ser Gln Ser Val
660 665 670

Gln Ser Lys Ile Leu Ala Phe Gly Leu Tyr Ala Gly Ser Ala Arg Leu
675 680 685

Tyr Cys Pro Gly Lys Leu Pro Phe Leu
690 695

<210> 49

<211> 2112

<212> DNA

<213> Neisseria meningitidis

<400> 49

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<210> 50

<211> 703

<212> PRT

<213> Neisseria meningitidis

<400> 50

Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala

1

5

10

15

Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr

20

25

30

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser

35

40

45

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn

50

55

60

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile

65

70

75

80

Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu

85

90

95

Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile

100	105	110
Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly		
115	120	125
Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg		
130	135	140
Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn		
145	150	155
Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln		
165	170	175
Ser Arg Asn Ile Gly Ala Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu		
180	185	190
Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu		
195	200	205
Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser		
210	215	220
Lys Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly		
225	230	235
Leu Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro		
245	250	255
Asp Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr		
260	265	270
Arg Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln		
275	280	285
Val Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala		
290	295	300
Gln Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe		
305	310	315
Tyr Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp		
325	330	335
Gln Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Phe Thr Leu Asn Gly		
340	345	350
Asp Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp		

355

360

365

Tyr Ser Arg Glu His Arg Asn Pro Thr Leu Gly Tyr Ser Arg Ala Phe
370 375 380

Thr Ala Ser Ile Asp Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly
385 390 395 400

Arg Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr
405 410 415

Gly Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe
420 425 430

Val Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys
435 440 445

Leu Thr Gly Ser Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn
450 455 460

Ile Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser
465 470 475 480

Tyr Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser
485 490 495

Ile Asn Thr Ser Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr
500 505 510

Arg Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu
515 520 525

Ser Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr
530 535 540

Arg Pro Asp Glu Gln Asn Asp Pro Tyr Thr Trp Ala Val Gly Gly Lys
545 550 555 560

His Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro
565 570 575

Lys Lys Leu Tyr Leu Arg Gly Ser Leu Gly Val Met Gln Ala Lys Val
580 585 590

Val Glu Asp Lys Glu Asn Pro Asp Arg Val Gly Ile His Leu Asn Asn
595 600 605

Thr Ser Asn Val Thr Gly Asn Leu Phe Phe Arg Tyr Thr Pro Thr Glu

610 615 620
 Asn Leu Tyr Gly Glu Ile Gly Val Thr Gly Thr Gly Lys Arg Tyr Gly
 625 630 635 640
 Tyr Asn Ser Arg Asn Lys Glu Val Thr Thr Leu Pro Gly Phe Ala Arg
 645 650 655
 Val Asp Ala Met Leu Gly Trp Asn His Lys Asn Val Asn Ile Thr Phe
 660 665 670
 Ala Ala Ala Asn Leu Leu Asn Gln Lys Tyr Trp Arg Ser Asp Ala Met
 675 680 685
 Pro Gly Ala Pro Arg Thr Tyr Thr Ala Arg Val Asn Tyr Ser Phe
 690 695 700

<210> 51

<211> 2112

<212> DNA

<213> Neisseria meningitidis

<400> 51

atgaaaatat catttcattt agctttatta cccacgctga ttattgcttc cttccctggt 60
 gctgccgccg atacgcagga caatggtgaa cattacaccg ccactctgcc caccgtttcc 120
 gtggtcggac agtccgacac cagcgtactc aaaggctaca tcaactacga cgaagccgcc 180
 gttacccgca acggacagct catcaaagaa acgccgcaaa ccatcgatac gctcaatatc 240
 cagaaaaaca aaaattacgg tacgaacgat ttgagttcca tcctcgaagg caatgccggc 300
 atcgacgctg cctacgatat gcgcggtgaa agcattttcc tgcgcggttt tcaagccgac 360
 gcatccgata tttaccgcca cggcgtgcgc gaaagcggac aagtgcgccg cagtactgcc 420
 aacatcgagc gcgtggaaat cctgaaaggc cgtcttccg tgctttacgg ccgcaccaac 480
 ggcggcggcg tcatcaacat ggtcagcaaa tacgccaaact tcaaacaag cgcgaacatc 540
 ggagcgggtt acggctcatg ggcaaacgc agcctgaata tggacattaa cgaagtgtcg 600
 aacaaaaacg tcgccatccg tctcaccggc gaagtcgggc gcgccaatc gttccgcagc 660
 ggcatagaca gcaaaaatgt catggtttcg cccagcatta ccgtcaaact cgacaacggc 720
 ttgaagtgga cggggcaata cacctacgac aatgtggagc gcacgcccca ccgcagtccg 780
 accaagtccg tgtacgaccg cttcggactg ccttaccgca tggggttcgc ccaccggaac 840
 gattttgtca aagacaagct gcaagtttg cgttccgacc ttgaatacgc cttcaacgac 900
 aaatggcgtg cccaatggca gtcgcccac cgcacggcgg cgcaggattt tgatcatttc 960
 tatgcaggca gcgaaaatgg caacttaatc aaacgtaact acgcctggca gcagaccgac 1020
 aacaaaaccc tgtcgtccaa cttaacgctc aacggcgact acaccatcg ccgttttgaa 1080
 aaccacctga ccgtaggcat ggattacagc cgcgaacacc gcaaccggac attgggtttc 1140
 agcagcgcc tttccgctc catcaacccc tacgaccggc caagctggcc ggcttcgggc 1200
 agattgcagc ctattctgac ccaaaaccgc cacaagccg actcctacgg catctttgtg 1260
 caaaacatct tctccgccac gcccgatttg aaattcgtcc tcggcggccg ttacgacaaa 1320
 tacaccttta attccgaaaa caaactcacc ggcagcagcc gccataacag cggacactcg 1380
 ttcagcccca acatcggcgc agtgtggaac atcaatcccg tocacacact ttacgcctcg 1440

tataacaaag gcttcgcgcc ttatggcgga cgcggcggtt atttgagcat cgatacgttg 1500
 tcttccgccg tggtcaacgc cgaccccgag tacacccgcc aatacgaaac cggcgtgaaa 1560
 agcagttggc tggacgaccg cctcagcact acgttggtctg cctaccaaata cgaacgcttc 1620
 aatatccgct accgccccga tccaaaaaac aacccttata tttatgcggt tagcggcaaa 1680
 caccgttcgc gcggcggtga attgtccgcc atcggggcaaa tcatcccaa aaaactctat 1740
 ctgcgcggtt cggtgggcgt gatgcaggcg aaagtgcgtt aagacaaaga aaatcccgcac 1800
 cgagtgggca tccatttgaa taataccagc aacgttaccg gcaacctgtt tttccgttat 1860
 accccgaccg aaaacctcta cggcgaaatc ggcgtaaccg gtacaggcaa acgctacggt 1920
 tacaactcaa gaaataaaga agtgactacg cttccaggct ttgcccagat tgatgccatg 1980
 cttggctgga accataaaaa tgtaacggtt acctttgcgc cagccaatct gctcaatcaa 2040
 aaatattggc gttcggactc tatgccgggt aatccgcgcg gctatactgc ccgggtaaat 2100
 taccgtttct ga 2112

<210> 52

<211> 703

<212> PRT

<213> Neisseria meningitidis

<400> 52

Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
 1 5 10 15

Ser Phe Pro Val Ala Ala Ala Asp Thr Gln Asp Asn Gly Glu His Tyr
 20 25 30

Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
 35 40 45

Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
 50 55 60

Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
 65 70 75 80

Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu
 85 90 95

Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile
 100 105 110

Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly
 115 120 125

Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg
 130 135 140

Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn
 145 150 155 160

Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln
 165 170 175
 Ser Arg Asn Ile Gly Ala Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu
 180 185 190
 Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu
 195 200 205
 Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser
 210 215 220
 Lys Asn Val Met Val Ser Pro Ser Ile Thr Val Lys Leu Asp Asn Gly
 225 230 235 240
 Leu Lys Trp Thr Gly Gln Tyr Thr Tyr Asp Asn Val Glu Arg Thr Pro
 245 250 255
 Asp Arg Ser Pro Thr Lys Ser Val Tyr Asp Arg Phe Gly Leu Pro Tyr
 260 265 270
 Arg Met Gly Phe Ala His Arg Asn Asp Phe Val Lys Asp Lys Leu Gln
 275 280 285
 Val Trp Arg Ser Asp Leu Glu Tyr Ala Phe Asn Asp Lys Trp Arg Ala
 290 295 300
 Gln Trp Gln Leu Ala His Arg Thr Ala Ala Gln Asp Phe Asp His Phe
 305 310 315 320
 Tyr Ala Gly Ser Glu Asn Gly Asn Leu Ile Lys Arg Asn Tyr Ala Trp
 325 330 335
 Gln Gln Thr Asp Asn Lys Thr Leu Ser Ser Asn Leu Thr Leu Asn Gly
 340 345 350
 Asp Tyr Thr Ile Gly Arg Phe Glu Asn His Leu Thr Val Gly Met Asp
 355 360 365
 Tyr Ser Arg Glu His Arg Asn Pro Thr Leu Gly Phe Ser Ser Ala Phe
 370 375 380
 Ser Ala Ser Ile Asn Pro Tyr Asp Arg Ala Ser Trp Pro Ala Ser Gly
 385 390 395 400
 Arg Leu Gln Pro Ile Leu Thr Gln Asn Arg His Lys Ala Asp Ser Tyr
 405 410 415

Gly Ile Phe Val Gln Asn Ile Phe Ser Ala Thr Pro Asp Leu Lys Phe
 420 425 430

Val Leu Gly Gly Arg Tyr Asp Lys Tyr Thr Phe Asn Ser Glu Asn Lys
 435 440 445

Leu Thr Gly Ser Ser Arg Gln Tyr Ser Gly His Ser Phe Ser Pro Asn
 450 455 460

Ile Gly Ala Val Trp Asn Ile Asn Pro Val His Thr Leu Tyr Ala Ser
 465 470 475 480

Tyr Asn Lys Gly Phe Ala Pro Tyr Gly Gly Arg Gly Gly Tyr Leu Ser
 485 490 495

Ile Asp Thr Leu Ser Ser Ala Val Phe Asn Ala Asp Pro Glu Tyr Thr
 500 505 510

Arg Gln Tyr Glu Thr Gly Val Lys Ser Ser Trp Leu Asp Asp Arg Leu
 515 520 525

Ser Thr Thr Leu Ser Ala Tyr Gln Ile Glu Arg Phe Asn Ile Arg Tyr
 530 535 540

Arg Pro Asp Pro Lys Asn Asn Pro Tyr Ile Tyr Ala Val Ser Gly Lys
 545 550 555 560

His Arg Ser Arg Gly Val Glu Leu Ser Ala Ile Gly Gln Ile Ile Pro
 565 570 575

Lys Lys Leu Tyr Leu Arg Gly Ser Leu Gly Val Met Gln Ala Lys Val
 580 585 590

Val Glu Asp Lys Glu Asn Pro Asp Arg Val Gly Ile His Leu Asn Asn
 595 600 605

Thr Ser Asn Val Thr Gly Asn Leu Phe Phe Arg Tyr Thr Pro Thr Glu
 610 615 620

Asn Leu Tyr Gly Glu Ile Gly Val Thr Gly Thr Gly Lys Arg Tyr Gly
 625 630 635 640

Tyr Asn Ser Arg Asn Lys Glu Val Thr Thr Leu Pro Gly Phe Ala Arg
 645 650 655

Val Asp Ala Met Leu Gly Trp Asn His Lys Asn Val Asn Val Thr Phe
 660 665 670

Ala Ala Ala Asn Leu Leu Asn Gln Lys Tyr Trp Arg Ser Asp Ser Met
 675 680 685

Pro Gly Asn Pro Arg Gly Tyr Thr Ala Arg Val Asn Tyr Arg Phe
 690 695 700

<210> 53

<211> 693

<212> DNA

<213> Neisseria meningitidis

<400> 53

atgaaacgct tcacctatac tctttccgac ggcttgtgca tcgaaatcga actcaaacgc 60
 agtgccaaga aaaatctgat tctgcgcccc gtcaatatgc agacgggtcag catcaacgtc 120
 ccaccctttt ttcaagacca cgcgttagca aactggctgg cggcaaacga aacgattttg 180
 cggaacacgc ttgctaaaat gcccggtgat cctgtttccc acccaaactt acccgagtgg 240
 atttgggtatc ggggaataaaa gaccaagctg gatacccaca gccaaagcca tatccgtatc 300
 acgtcgtctg aaatcctgct tccccgaaaa gaaaccgccg cacaaatcga ccacctgcgc 360
 cgctgtttga acgaacgcgc ccgcgaatac ctgctgcccc gccttgaaaa acacgcagcc 420
 gaaacaggac tgactcccgc tgccacagac ctgagcaacg ccaaaacctt ttggggcgta 480
 tgccgcccgc acaccggcat ccgcctcaac tggcgggtga tcggcacgcc cgaatacgtc 540
 gccgactatg tctgcatcca cgaactctgc cacctccgcc accccgacca cagtccgcgc 600
 ttttggcatt tgggtgaacac gctgacgccg cataccgaca atgctaaaag ttggctgaag 660
 gcgcacgggc ggggaattggt tgtgctgggg taa 693

<210> 54

<211> 230

<212> PRT

<213> Neisseria meningitidis

<400> 54

Met Lys Arg Phe Thr Tyr Thr Leu Ser Asp Gly Leu Cys Ile Glu Ile
 1 5 10 15

Glu Leu Lys Arg Ser Ala Lys Lys Asn Leu Ile Leu Arg Pro Val Asn
 20 25 30

Met Gln Thr Val Ser Ile Asn Val Pro Pro Phe Phe Gln Asp His Ala
 35 40 45

Leu Ala Asn Trp Leu Ala Ala Asn Glu Thr Ile Leu Arg Asn Thr Leu
 50 55 60

Ala Lys Met Pro Val His Pro Val Ser His Pro Asn Leu Pro Glu Trp
 65 70 75 80

Ile Trp Tyr Arg Gly Ile Lys Thr Lys Leu Asp Thr His Ser Gln Ser
85 90 95

His Ile Arg Ile Thr Ser Ser Glu Ile Leu Leu Pro Arg Lys Glu Thr
100 105 110

Ala Ala Gln Ile Asp His Leu Arg Arg Leu Leu Asn Glu Arg Ala Arg
115 120 125

Glu Tyr Leu Leu Pro Arg Leu Glu Lys His Ala Ala Glu Thr Gly Leu
130 135 140

Thr Pro Ala Ala Thr Asp Leu Ser Asn Ala Lys Thr Phe Trp Gly Val
145 150 155 160

Cys Arg Pro His Thr Gly Ile Arg Leu Asn Trp Arg Leu Ile Gly Thr
165 170 175

Pro Glu Tyr Val Ala Asp Tyr Val Cys Ile His Glu Leu Cys His Leu
180 185 190

Arg His Pro Asp His Ser Pro Arg Phe Trp His Leu Val Asn Thr Leu
195 200 205

Thr Pro His Thr Asp Asn Ala Lys Ser Trp Leu Lys Ala His Gly Arg
210 215 220

Glu Leu Phe Val Leu Gly
225 230

<210> 55

<211> 546

<212> DNA

<213> Neisseria meningitidis

<400> 55

atgagcaaga ttattgtgct gaccgcaggc cacagcaaca ccgacccggg tgcggtcaac 60
ggaagcgacc gtgaggcgga cttggcgag gatatgcgca acattgtggc ttcaatcctg 120
cgtaacgatt acggcctgac cgtaaacc gacggcacgg gcaaaggcaa tatgccgctg 180
cgcgaaagcgg tcaagctgat tcgcggtcg gatgtggcga ttgagtttca caccaacgct 240
gccgtcagca aagcggcgac aggcacgaa gccttgagta ccgttaaaaa caaacgctgg 300
tgtcagggtgt tgagcaaagc cgttgccaaag aaaaccggct ggaaactgcg cggcgaagac 360
ggctttaaac ccgacaatgc gggccagcat tcgcgcctgg cttatgcaca agccggcggc 420
attgtgtttg agcctttttt catcagcaac gacactgatt tggccttggt taagacgact 480
aaatggggca tctgccgcgc gattgcggac gcgattgcga tggaattggg ggcggaaga 540
gtatga 546

<210> 56
 <211> 181
 <212> PRT
 <213> Neisseria meningitidis

<400> 56

Met Ser Lys Ile Ile Val Leu Thr Ala Gly His Ser Asn Thr Asp Pro
 1 5 10 15

Gly Ala Val Asn Gly Ser Asp Arg Glu Ala Asp Leu Ala Gln Asp Met
 20 25 30

Arg Asn Ile Val Ala Ser Ile Leu Arg Asn Asp Tyr Gly Leu Thr Val
 35 40 45

Lys Thr Asp Gly Thr Gly Lys Gly Asn Met Pro Leu Arg Glu Ala Val
 50 55 60

Lys Leu Ile Arg Gly Ser Asp Val Ala Ile Glu Phe His Thr Asn Ala
 65 70 75 80

Ala Val Ser Lys Ala Ala Thr Gly Ile Glu Ala Leu Ser Thr Val Lys
 85 90 95

Asn Lys Arg Trp Cys Gln Val Leu Ser Lys Ala Val Ala Lys Lys Thr
 100 105 110

Gly Trp Lys Leu Arg Gly Glu Asp Gly Phe Lys Pro Asp Asn Ala Gly
 115 120 125

Gln His Ser Arg Leu Ala Tyr Ala Gln Ala Gly Gly Ile Val Phe Glu
 130 135 140

Pro Phe Phe Ile Ser Asn Asp Thr Asp Leu Ala Leu Phe Lys Thr Thr
 145 150 155 160

Lys Trp Gly Ile Cys Arg Ala Ile Ala Asp Ala Ile Ala Met Glu Leu
 165 170 175

Gly Ala Ala Arg Val
 180

<210> 57
 <211> 237
 <212> DNA
 <213> Neisseria meningitidis

<400> 57

atgcggtatatt tggatatttt taaaaaccca gcgacaggca atgtgtcgca ctcgaaactg 60
 tgggcaaacg ttgcctgcgc ggcggggacg gttaagtttg tgatgctgcc cgacccgtcg 120
 gcgagatatt gggcggtgta tttgggcatt gtcggcggt atgcggtggc gcgttcgttg 180
 gtcagcgta aacgtcagga ggtcgagaat gaatctcgtg aaactgctgg cgaataa 237

<210> 58

<211> 78

<212> PRT

<213> Neisseria meningitidis

<400> 58

Met Arg Ile Leu Asp Ile Phe Lys Asn Pro Ala Thr Gly Asn Val Ser
 1 5 10 15

His Ser Lys Leu Trp Ala Asn Val Ala Cys Ala Ala Gly Thr Val Lys
 20 25 30

Phe Val Met Leu Pro Asp Pro Ser Ala Glu Ile Trp Ala Val Tyr Leu
 35 40 45

Gly Ile Val Gly Gly Tyr Ala Val Ala Arg Ser Leu Val Ser Val Lys
 50 55 60

Arg Gln Glu Val Glu Asn Glu Ser Arg Glu Thr Ala Gly Glu
 65 70 75

<210> 59

<211> 468

<212> DNA

<213> Neisseria meningitidis

<400> 59

atgcggtggc gcgttcgttg gtcagcgta aacgtcagga ggtcgagaat gaatctcgtg 60
 aaactgctgg cgaataactg gcaaccgatt gccatcatcg cgcttgctcg caggggttg 120
~~gcggtgtcgc accatcaagg ctacaagtcg gctttttgga agcagcagge ggteattgag 180~~
 aaaatgaagc gcgacaaggc gcaagccctg ctggtgtcgg ctcaaaacta cgcccgcgaa 240
 ctggaacagg cgcgtgcgga agctaaaaaa tatgaagtca aggcgcacgc cgtcggcatg 300
 gctttggcga aaaaacaggc ggaagtcagc cgtctgaaaa cggaaaataa aaaggaaatc 360
 gaaaatgtcc ttactcaaga ccgtaaaaat gcaggcggcg gttgtattga cggctttggc 420
 catcacggct tgcagctcta caagcgcgcc ctcggctacg gaaattaa 468

<210> 60

<211> 155

<212> PRT

<213> Neisseria meningitidis

<400> 60

Met Arg Trp Arg Val Arg Trp Ser Ala Ser Asn Val Arg Arg Ser Arg
 1 5 10 15

Met Asn Leu Val Lys Leu Leu Ala Asn Asn Trp Gln Pro Ile Ala Ile
 20 25 30

Ile Ala Leu Val Gly Thr Gly Leu Ala Val Ser His His Gln Gly Tyr
 35 40 45

Lys Ser Ala Phe Ala Lys Gln Gln Ala Val Ile Glu Lys Met Lys Arg
 50 55 60

Asp Lys Ala Gln Ala Leu Leu Leu Ser Ala Gln Asn Tyr Ala Arg Glu
 65 70 75 80

Leu Glu Gln Ala Arg Ala Glu Ala Lys Lys Tyr Glu Val Lys Ala His
 85 90 95

Ala Val Gly Met Ala Leu Ala Lys Lys Gln Ala Glu Val Ser Arg Leu
 100 105 110

Lys Thr Glu Asn Lys Lys Glu Ile Glu Asn Val Leu Thr Gln Asp Arg
 115 120 125

Lys Asn Ala Gly Gly Gly Cys Ile Asp Gly Phe Gly His His Gly Leu
 130 135 140

Gln Leu Tyr Lys Arg Ala Leu Gly Tyr Gly Asn
 145 150 155

<210> 61

<211> 306

<212> DNA

<213> *Neisseria meningitidis*

<400> 61

atgtccttac tcaagaccgt aaaaatgcag gcggcggttg tattgacggc tttggccatc 60
 acggcttgca gctctacaag cgcgccctcg gctacggaaa ttaagggtgt cgaaaaggcg 120
 gtcattgccga caccgcctgc cgcgttgatg gtcgcgccgg tgcgcccgaa tccgccgaaa 180
 gacggcaaga cggccacgct gttggaacac gccgccgagt ttggcggcta tgttgccgaa 240
 cttgaaaacc aaaatcaggc ttggcgcgac tgggcgggca atcactcccg caaagtcgga 300
 aactga 306

<210> 62

<211> 101

<212> PRT

<213> Neisseria meningitidis

<400> 62

Met Ser Leu Leu Lys Thr Val Lys Met Gln Ala Ala Val Val Leu Thr
 1 5 10 15

Ala Leu Ala Ile Thr Ala Cys Ser Ser Thr Ser Ala Pro Ser Ala Thr
 20 25 30

Glu Ile Lys Val Val Glu Lys Ala Val Met Pro Thr Pro Pro Ala Ala
 35 40 45

Leu Met Val Ala Pro Val Arg Pro Asn Pro Pro Lys Asp Gly Lys Thr
 50 55 60

Ala Thr Leu Leu Glu His Ala Ala Glu Phe Gly Gly Tyr Val Ala Glu
 65 70 75 80

Leu Glu Asn Gln Asn Gln Ala Trp Arg Asp Trp Ala Gly Asn His Ser
 85 90 95

Arg Lys Val Gly Asn
 100

<210> 63

<211> 348

<212> DNA

<213> Neisseria meningitidis

<400> 63

gtgctggcag ttttgcttgc tgggtgtagcc ttcgccctga gcgatgattt catggttggc 60
 tgctttcaaa cgccaacggt attcgccctt tgcgtcttta tagatttcaa aatacataag 120
 gtttctccta tgaatgagta cacgttttct taccgcttta acggcaagtc ctggtcattg 180
 agcatttggg cggacaaccc tgaagaagcc agggcgaaat ttcgggctgc acgagaaaat 240
 ggcgactatg acggcggaagt tgtagcaaag gtttatacat ttgtaaatat ttcgtggggt 300
 aagaaattgt acaagcggac aaaatattta atgggtatca aagaatga 348

<210> 64

<211> 115

<212> PRT

<213> Neisseria meningitidis

<400> 64

Val Leu Ala Val Leu Leu Ala Gly Val Ala Phe Ala Leu Ser Asp Asp
 1 5 10 15

Phe Met Val Gly Cys Phe Gln Thr Pro Thr Val Phe Ala Phe Cys Val
 20 25 30

Phe Ile Asp Phe Lys Ile His Lys Val Ser Pro Met Asn Glu Tyr Thr
 35 40 45

Phe Ser Tyr Arg Phe Asn Gly Lys Ser Trp Ser Leu Ser Ile Trp Ala
 50 55 60

Asp Asn Pro Glu Glu Ala Arg Ala Lys Phe Arg Ala Ala Arg Glu Asn
 65 70 75 80

Ala His Tyr Asp Gly Glu Val Val Ala Lys Val Tyr Thr Phe Val Asn
 85 90 95

Ile Ser Trp Val Lys Lys Leu Tyr Lys Arg Thr Lys Tyr Leu Met Gly
 100 105 110

Ile Lys Glu
 115

<210> 65

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<400> 65

atgacattgc tcaatctaata gataatgcaa gattacggta tttccgtttg cctgacactg 60
 acgccctatt tgcaacatga actatttttcg gctatgaaat cctatttttc caaatatatac 120
 ctaccggttt cactttttac cttgccacta tccctttccc catccgtttc ggcttttacg 180
 ctgcctgaag catggcgggc ggcgagcaa cattcggtcg attttcaagc gtcccattac 240
 cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
 tccgccaatg ccagctacca gcgccagccg ccatcgattt cttccaccgc cgaaacacag 360
 ggatggagcg tgcaggtggg acaaacctta tttgacgtcg ccaaatttgc acaataccgc 420
 caaagcaggt tcgatacgca ggctgcagaa cagcgtttcg atgcggcacg cgaagaattg 480
 ctgttgaaag ttgccgaaag ttatttcaac gttttactca gccgagacac cgttgccgcc 540
 catgcggcgg aaaaagaggg ttatgccag caggtaaggc aggcgcaggc tttattcaat 600
 aaaggtgctg ccaccgcgct ggatattcac gaagccaaag ccggttacga caatgccctg 660
 gcccaagaaa tcgccgtatt ggctgagaaa caaacctatg aaaaccagtt gaacgactac 720
 accggcctgg acagcaaaca aatcgaggcc atagataccg ccaacctgtt ggcacgctat 780
 ctgcccagc tggaacgtta cagtctggat gaatggcagc gcattgcctt atccaacaat 840
 catgaatacc ggatgcagca gcttgccctg caaagcagcg gacaggcgct tcgggcagca 900
 cagaacagcc gctatcccac cgtttctgcc catgtcggct atcagaataa cctctacact 960
 tcattctgcg agaataatga ctaccactat cggggcaaag ggatgagcgt cggcgtagac 1020
 ttgaatttgc cgctttatac cggcggagaa ttgtcgggca aaatccatga agccgaagcg 1080
 caatacggg ctgccgaagc acagctgacc gcaaccgagc ggcacatcaa actcgccgta 1140
 cgccaggctt ataccgaaag cgggtgcggcg cgttacaaa tcatggcgca agaacggggt 1200

ttggaaagca gccgtttgaa actgaaatcg accgaaaccg gccacaata cggcatccgc 1260
 aaccggctgg aagtaatacg ggcgcggcag gaagtcgccc aagcagaaca gaaactggct 1320
 caagcacggt ataaattcat gctggcttat ttgcgcttgg tgaaagagag cgggttaggg 1380
 ttggaaacgg tatttgcgga ataa 1404

<210> 66

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 66

Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
 1 5 10 15

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
 115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
 130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
 145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
 165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
 180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp

195

200

205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
 210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
 225 230 235 240

Thr Gly Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
 245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
 260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
 275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
 290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
 305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
 325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
 340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
 355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
 370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
 385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
 405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
 420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
 435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val

450

455

460

Phe Ala Glu

465

<210> 67

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<400> 67

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cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
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```

<210> 68

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 68

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Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
  1             5             10             15

```

```

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
          20             25             30

```

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
225 230 235 240

Thr Gly Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
 290 295 300
 Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
 305 310 315 320
 Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
 325 330 335
 Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
 340 345 350
 Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
 355 360 365
 Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
 370 375 380
 Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
 385 390 395 400
 Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
 405 410 415
 Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
 420 425 430
 Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
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 Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
 450 455 460
 Phe Ala Glu
 465

<210> 69

<211> 1400

<212> DNA

<213> Neisseria meningitidis

<400> 69

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 ccgtttcact ttttaccttg ccactatccc tttccccatc cgtttcggct tttacgctgc 180
 ctgaagcatg gcgggcggcg cagcaacatt cggtgattt tcaagcgtcc cattaccagc 240

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gtgatgcagt ggcgcacg cacaacaag ccaaggccgc attccttccc catgtatccg 300
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ggagcgtgca ggtgggacaa accttatttg actctgccaa atttgcacaa taccgccaaa 420
gcaggttcga tacgcaggct gcagaacagc gtttcgatgc ggcacgcgaa gaattgctgt 480
tgaaagttgc cgaaagttat ttcaacgttt tactcagccg agacaccgtt gccgcccatg 540
cggcggaataa agaggcttat gccagcagg taaggcaggc gcaggcttta ttcaataaag 600
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aagaaatcgc cgtattggct gagaaacaaa cctatgaaaa ccagttgaac gactacaccg 720
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<210> 70

<211> 450

<212> PRT

<213> Neisseria meningitidis

<400> 70

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Met Thr Leu Leu Asn Leu Ile Cys Lys Ile Thr Val Phe Pro Phe Ala
  1              5              10              15

```

```

His Arg Pro Ile Cys Asn Met Asn Tyr Phe Arg Leu Asn Pro Ile Phe
      20              25              30

```

```

Pro Asn Ile Ser Tyr Pro Phe His Phe Leu Pro Cys His Tyr Pro Phe
      35              40              45

```

```

Pro His Pro Phe Arg Leu Leu Arg Cys Leu Lys His Gly Gly Arg Arg
      50              55              60

```

```

Ser Asn Ile Arg Leu Ile Phe Lys Arg Pro Ile Thr Ser Val Met Gln
      65              70              75              80

```

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Cys Ala His Gly Asn Asn Lys Pro Arg Pro His Ser Phe Pro Met Tyr
      85              90              95

```

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Pro Pro Met Pro Ala Thr Ser Ala Ser Arg His Arg Phe Leu Pro Pro
      100             105             110

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Ala Lys His Arg Asp Gly Ala Cys Arg Trp Asp Lys Pro Tyr Leu Thr
 115 120 125

Leu Pro Asn Leu His Asn Thr Ala Lys Ala Gly Ser Ile Arg Arg Leu
 130 135 140

Gln Asn Ser Val Ser Met Arg His Ala Lys Asn Cys Cys Lys Leu Pro
 145 150 155 160

Lys Val Ile Ser Thr Phe Tyr Ser Ala Glu Thr Pro Leu Pro Pro Met
 165 170 175

Arg Arg Lys Lys Arg Leu Met Pro Ser Arg Gly Arg Arg Arg Leu Tyr
 180 185 190

Ser Ile Lys Val Leu Pro Pro Arg Ile Phe Thr Lys Pro Lys Pro Val
 195 200 205

Thr Thr Met Pro Trp Pro Lys Lys Ser Pro Tyr Trp Leu Arg Asn Lys
 210 215 220

Pro Met Lys Thr Ser Thr Thr Thr Pro Ala Trp Thr Ala Asn Lys Ser
 225 230 235 240

Arg Pro Ile Pro Pro Thr Cys Trp His Ala Ile Cys Pro Ser Trp Asn
 245 250 255

Val Thr Val Trp Met Asn Gly Ser Ala Leu Pro Tyr Pro Thr Ile Met
 260 265 270

Asn Thr Gly Cys Ser Ser Leu Pro Cys Lys Ala Ala Asp Arg Arg Phe
 275 280 285

Gly Gln His Arg Thr Ala Ala Ile Pro Pro Phe Leu Pro Met Ser Ala
 290 295 300

Ile Arg Ile Thr Ser Thr Leu His Leu Arg Arg Ile Met Thr Thr Thr
 305 310 315 320

Ile Gly Ala Lys Gly Ala Ser Ala Tyr Ser Ile Cys Arg Phe Ile Pro
 325 330 335

Ala Glu Asn Cys Arg Ala Lys Ser Met Lys Pro Lys Arg Asn Thr Gly
 340 345 350

Leu Pro Lys His Ser Pro Gln Pro Ser Gly Thr Ser Asn Ser Pro Tyr
 355 360 365

Ala Arg Leu Ile Pro Lys Ala Val Arg Arg Val Thr Lys Ser Trp Arg
 370 375 380

Lys Asn Gly Phe Trp Lys Ala Ala Val Asn Asn Arg Pro Lys Pro Ala
 385 390 395 400

Asn Asn Thr Ala Ser Ala Thr Gly Trp Lys Tyr Gly Arg Gly Arg Lys
 405 410 415

Ser Pro Lys Gln Asn Arg Asn Trp Leu Lys His Gly Ile Asn Ser Cys
 420 425 430

Trp Leu Ile Cys Ala Trp Lys Arg Ala Gly Gly Trp Lys Arg Tyr Leu
 435 440 445

Arg Asn
 450

<210> 71

<211> 1404

<212> DNA

<213> *Neisseria meningitidis*

<400> 71

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 ctaccggttt cacttttttac cttgccacta tccctttccc catccgtttc ggcttttacg 180
 ctgcctgaag catggcgggc ggcgagcaa cattcggctg attttcaagc gtcccattac 240
 cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
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 ggatggagcg tgcaggtggg acaaacctta tttgacgctg ccaaatttgc acaataccgc 420
 caaagcaggt tcgatacgca ggctgcagaa cagcgtttcg atgcggcagc cgaagaattg 480
 ctgttgaaag ttgccgaaag ttatttcaac gttttactca gccgagacac cgttgccgcc 540
 catgcggcgcg aaaaagaggc ttatgcccg caggttaaggc aggcgcaggc tttattcaat 600
 aaaggtgctg ccaccgcgct ggatattcac gaagccaaaag ccggttacga caatgcctg 660
 gccaagaaa tcgccgtatt ggctgagaaa caaacctatg aaaaccagtt gaacgactac 720
 accgacctgg atagcaaaca aatcgaggcc atagataccg ccaacctgtt ggcacgctat 780
 ctgccaagc tggaacgtta cagtctggat gaatggcagc gcattgcctt atccaacaat 840
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1404

<210> 72

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 72

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Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
 115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
 130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
 145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
 165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
 180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
 195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile

210

215

220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
 225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
 245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
 260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
 275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
 290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
 305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
 325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
 340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
 355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
 370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
 385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
 405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
 420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
 435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
 450 455 460

Phe Ala Glu

465

<210> 73

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<400> 73

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ctacccggtt cactttttac cttgccacta tccctttccc catccgtttc ggctttttacg 180
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tccgccaatg ccagctacca gcgccagccg ccatcgattt cttccacccg cgaaacacag 360
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caaagcaggt tcgatacgca ggctgcagaa cagcgttttcg atgcggcacg cgaagaattg 480
ctgttgaaag ttgccgaaag ttatttcaac gttttactca gccgagacac cgttgccgcc 540
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aaagggtgctg ccaccgcgct ggatattcac gaagccaaag ccggttacga caatgccctg 660
gcccagaata tcgccgtatt ggctgagaaa caaacctatg aaaaccagtt gaacgactac 720
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<210> 74

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 74

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Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
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Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
      20             25             30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
  35             40             45

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85

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala ile Asp Thr Ala Asn Leu
245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
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Phe Ala Glu
465

<210> 75

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<400> 75

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ctacccgttt cactttttac cttgccacta tccctttccc catccgittc ggctttttacg 180
ctgcctgaag catggcgggc ggcgagcaa cattcggtg attttcaagc gtcccattac 240
cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
tccgccaatg ccagctacca gcgccagccg ccatcgattt cttccaccgc cgaaacacag 360
ggatggagcg tgcaggtggg acaaacctta tttgacgctg ccaaatttgc acaataccgc 420

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catgcggcgg aaaaagaggc ttatgccag caggttaaggc aggcgcaggc tttattcaat 600
aaaggtgctg ccaccgcgct ggatattcac gaagccaaag ccggttacga caatgccctg 660
gcccagaata tcgccgtatt ggctgagaaa caaacctatg aaaaccagtt gaacgactac 720
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caagcacggt ataaattcat gctggcttat ttgcgcttgg tgaaagagag cgggttaggg 1380
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<210> 76

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 76

```

Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
  1             5             10             15

```

```

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
      20             25             30

```

```

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
      35             40             45

```

```

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
      50             55             60

```

```

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
      65             70             75             80

```

```

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
      85             90             95

```

```

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
      100            105            110

```

```

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
      115            120            125

```

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460

Phe Ala Glu
465

<210> 77

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<400> 77

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ctaccggttt cacttttttac cttgccacta tccctttccc catccgtttc ggctttttacg 180
ctgcctgaag catggcgggc ggcgagcaa cattcggttg attttcaagc gtcccattac 240
cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
tccgccaatg ccagctacca gcgccagccg ccacgattt cttccaccgc cgaacacacag 360
ggatggagcg tgcaggtggg acaaacctta tttgacgctg ccaaatttgc acaataccgc 420
caaagcaggt tcgatacgca ggctgcagaa cagcgttttc atgcggcacg cgaagaattg 480
ctgttgaaag ttgccgaaag ttatttcaac gttttactca gccgagacac cgttgccgcc 540
catgcggcgg aaaaagaggc ttatgccagc caggttaaggc aggcgcaggc tttattcaat 600
aaaggtgctg ccaccgcgct ggatattcac gaagccaaag ccggtttacg caatgccctg 660
gccaagaaa tcgccgtatt ggctgagaaa caaacctatg aaaaccagtt gaacgactac 720
accgacctgg atagcaaaca aatcgaggcc atagataccg ccaacctgtt ggcacgctat 780
ctgccaagc tggaacgtta cagtctggat gaatggcagc gcattgcctt atccaacaat 840
catgaatacc ggatgcagca gcttgccctg caaagcagcg gacaggcgct tcgggcagca 900
cagaacagcc gctatccac cgtttctgcc catgtcggct atcagaataa cctctacact 960
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caatacgggg ccgccgaagc acagctgacc gcaaccgagc ggcacatcaa actcgccgta 1140
cgccaggctt ataccgaaag cggcgcgcg cgttaccaa tcatggcgca agaacgggtt 1200
ttggaaagca gccgtttgaa actgaaatcg accgaaaccg gccacaata cggcatccgc 1260
aaccggctgg aagtaatacg ggcgcgagc gaagtcgccc aagcagaaca gaaactggct 1320
caagcacggt ataaattcat gctggcttat ttgcgcttgg tgaaagagag cgggttaggg 1380

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ttggaaacgg tatttgcgga ataa

1404

<210> 78

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 78

Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
 1 5 10 15

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
 115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
 130 135 140

~~Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu~~
 145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
 165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
 180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
 195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile

210

215

220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
 225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
 245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
 260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
 275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
 290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
 305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
 325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
 340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
 355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
 370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
 385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
 405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
 420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
 435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
 450 455 460

Phe Ala Glu

465

<210> 79

<211> 1404

<212> DNA

<213> *Neisseria meningitidis*

<400> 79

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ctaccggttt cacttttttac cttgccacta tccctttccc catccgtttc ggctttttacg 180
ctgcctgaag catggcgggc ggcgagcaa cattcggtg attttcaagc gtcccattac 240
cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
tccgccaatg ccagctacca gcgccagccg ccatcgattt cttccacccg cgaaacacag 360
ggatggagcg tgcaggtggg acaaacctta tttgacgtg ccaaatttgc acaataccgc 420
caaagcaggt tgcatacgca ggctgcagaa cagcgtttcg atgcggcacg cgaagaattg 480
ctgttgaaag ttgccgaaag ttatttcaac gttttactca gccgagacac cgttgccgcc 540
catgcggcgg aaaaagaggc ttatgccag caggttaaggc aggcgcaggc tttattcaat 600
aaaggtgctg ccaccgcgct ggatattcac gaagccaaag ccggttacga caatgccctg 660
gcccaagaaa tcgccgtatt ggctgagaaa caaacctatg aaaaccagtt gaacgactac 720
accgacctgg atagcaaaca aatcgaggcc atagataccg ccaacctgtt ggcacgctat 780
ctgcccaagc tggaacgtta cagtctggat gaatggcagc gcattgcctt atccaacaat 840
catgaatacc ggatgcagca gcttgccctg caaagcagcg gacaggcgct tcgggcagca 900
cagaacagcc gctatccac cgtttctgcc catgtcggct atcagaataa cctctacact 960
tcactctgcg agaataatga ctaccactat cggggcaaag ggatgagcgt cggcgtacag 1020
ttgaatttgc cgcttttatac cggcgagaa ttgtcgggca aaatccatga agccgaagcg 1080
caatacgggg ccgccgaagc acagctgacc gcaaccgagc ggcacatcaa actcgccgta 1140
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ttggaaagca gccgtttgaa actgaaatcg accgaaaccg gccacaata cggcatccgc 1260
aaccggctgg aagtaatacg ggcgcgagc gaagtgcgcc aagcagaaca gaaactggct 1320
caagcacggg ataaattcat gctggcttat ttgcgcttg tgaaagagag cgggttaggg 1380
ttggaaacgg tatttgcgga ataa 1404

```

<210> 80

<211> 467

<212> PRT

<213> *Neisseria meningitidis*

<400> 80

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Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
 1             5             10            15

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
      20             25            30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35             40            45

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Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
  50                      55                      60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
  65                      70                      75                      80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
                      85                      90                      95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
      100                      105                      110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
      115                      120                      125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
      130                      135                      140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
      145                      150                      155                      160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
      165                      170                      175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
      180                      185                      190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
      195                      200                      205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
      210                      215                      220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
      225                      230                      235                      240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
      245                      250                      255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
      260                      265                      270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
      275                      280                      285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
      290                      295                      300

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Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
 305 310 315 320
 Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
 325 330 335
 Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
 340 345 350
 Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
 355 360 365
 Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
 370 375 380
 Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
 385 390 395 400
 Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
 405 410 415
 Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
 420 425 430
 Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
 435 440 445
 Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
 450 455 460
 Phe Ala Glu
 465

<210> 81
 <211> 1404
 <212> DNA
 <213> Neisseria meningitidis

<400> 81
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 acgccctatt tgcaacatga actattttcg gctatgaaat cctatttttc caaatatata 120
 ctaccggttt cactttttac cttgccacta tccctttccc catccgtttc ggctttttacg 180
 ctgcctgaag catggcgggc ggcgagcaa cattcggtg attttcaagc gtccattac 240
 cagcgtgatg cagtgcgcgc acggcaaaa caagccaagg ccgcattcct tccccatgta 300
 tccgccaatg ccagctacca gcgccagccg ccatcgattt cttccaccgc cgaaacacag 360

```

ggatggagcg tgcaggtggg acaaacctta tttgacgctg ccaaatttgc acaataccgc 420
caaagcaggt tcgatacgca ggctgcagaa cagcgtttcg atgcggcacg cgaagaattg 480
ctggtgaaag ttgccgaaag ttatttcaac gttttactca gccgagacac cgttgccgcc 540
catgcggcgg aaaaagaggc ttatgccag caggtaaggc aggcgcaggc tttattcaat 600
aaaggtgctg ccaccgcgct ggatattcac gaagccaaag ccggttacga caatgccctg 660
gcccaagaaa tcgccgtatt ggctgagaaa caaacctatg aaaaccagtt gaacgactac 720
accgacctgg atagcaaaca aatcgaggcc atagataccg ccaacctgtt ggcacgctat 780
ctgccccagc tggaacgtta cagtctggat gaatggcagc gcattgcctt atccaacaat 840
catgaatacc ggatgcagca gcttgccctg caaagcagcg gacaggcgct tcgggcagca 900
cagaacagcc gctatcccac cgtttctgcc catgtcggct atcagaataa cctctacact 960
tcatctgcgc agaataatga ctaccactat cggggcaaaag ggatgagcgt cggcgtagag 1020
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caatacgggg ccgccgaagc acagctgacc gcaaccgagc ggcacatcaa actcgccgta 1140
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caagcacggt ataaattcat gctggcttat ttgcgcttg tgaaagagag cgggttaggg 1380
ttggaaacgg tatttgcgga ataa 1404

```

<210> 82

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 82

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Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
  1                      5                      10                      15

```

```

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
      20                      25                      30

```

```

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
    35                      40                      45

```

```

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
    50                      55                      60

```

```

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
    65                      70                      75                      80

```

```

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
      85                      90                      95

```

```

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
    100                      105                      110

```

```

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
    115                      120                      125

```

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460

Phe Ala Glu
465

<210> 83

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<400> 83

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ctaccggttt cactttttac cttgccacta tccctttccc catccgtttc ggctttttacg 180
ctgcctgaag catggcgggc ggcgcagcaa cattcggctg attttcaagc gtcccattac 240
cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
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ggatggagcg tgcaggtggg acaaacctta tttgacgctg ccaaatttgc acaataccgc 420
caaagcaggt tcgatacgca ggctgcagaa cagcgtttcg atgcggcacg cgaagaattg 480
ctgttgaaag ttgccgaaag ttattttcaac gttttactca gccgagacac cgttgccgcc 540
catgcggcgg aaaaagaggc ttatgcccag caggtaaggc aggcgcaggc tttattcaat 600
aaagggtgctg ccaccgcgct ggatattcac gaagccaaag ccggttacga caatgccctg 660
gcccaagaaa tcgccgtatt ggctgagaaa caaacctatg aaaaccagtt gaacgactac 720
accgacctgg atagcaaaca aatcgaggcc atagataccg ccaacctgtt ggacgctat 780
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cagaacagcc gctatccac cgttttctgcc catgtcggct atcagaataa cctctacact 960
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aaccggctgg aagtaatacg ggcgcggcag gaagtcgccc aagcagaaca gaaactggct 1320

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caagcacggt ataaattcat gctggcttat ttgcgcttgg tgaaagagag cgggttaggg 1380
 ttggaaacgg tatttgcgga ataa 1404

<210> 84

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 84

Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
 1 5 10 15

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
 115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
 130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
 145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
 165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
 180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
 195 200 205

```

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
  210                      215                      220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
  225                      230                      235                      240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
      245                      250                      255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
      260                      265                      270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
      275                      280                      285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
      290                      295                      300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
  305                      310                      315                      320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
      325                      330                      335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
      340                      345                      350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
      355                      360                      365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
      370                      375                      380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
  385                      390                      395                      400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
      405                      410                      415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
      420                      425                      430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
      435                      440                      445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
      450                      455                      460

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Phe Ala Glu

465

<210> 85

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<400> 85

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ctacccgttt cactttttac cttgccacta tccctttccc catccgtttc ggctttttacg 180
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cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
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ggatggagcg tgcaggtggg acaaacctta ttgacgctg ccaaatttgc acaataccgc 420
caaagcaggt tgcatacgca ggctgcagaa cagcgtttcg atgcggcacg cgaagaattg 480
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aaaggtgctg ccaccgcgct ggatattcac gaagccaaag ccggttacga caatgccctg 660
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<210> 86

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 86

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Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
  1             5             10             15

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
      20             25             30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu

```

35	40	45
Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala		
50	55	60
Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr		
65	70	75 80
Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe		
85	90	95
Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser		
100	105	110
Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln		
115	120	125
Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe		
130	135	140
Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu		
145	150	155 160
Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp		
165	170	175
Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val		
180	185	190
Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp		
195	200	205
Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile		
210	215	220
Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr		
225	230	235 240
Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu		
245	250	255
Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp		
260	265	270
Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu		
275	280	285
Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg		

290

295

300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
 305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
 325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
 340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
 355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
 370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
 385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
 405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
 420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
 435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
 450 455 460

Phe Ala Glu
 465

<210> 87

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<400> 87

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 cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
 tccgccaatg ccagctacca gcgccagccg ccatcgattt cttccaccgc cgaaacacag 360

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catgcggcgg aaaaagaggc ttatgcccag caggtaaggc aggcgcaggc tttattcaat 600
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gccccagaaa tcgccgtatt ggctgagaaa caaacctatg aaaaccagtt gaacgactac 720
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caagcacggt ataaattcat gctggcttat ttgcgcttgg tgaaagagag cggggttaggg 1380
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<210> 88

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 88

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Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
  1              5              10             15

```

```

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
      20              25             30

```

```

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
      35              40             45

```

```

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
      50              55             60

```

```

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
      65              70             75             80

```

```

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
      85              90             95

```

```

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
      100             105            110

```

```

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
      115             120            125

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Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460

Phe Ala Glu
465

<210> 89

<211> 1404

<212> DNA

<213> Neisseria meningitidis

<400> 89

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ctacccggtt cacttttttac cttgccacta tccctttccc catccgtttc ggcttttaacg 180
ctgcctgaag catggcgggc ggccgcagcaa cattcggctg attttcaagc gtcccattac 240
cagcgtgatg cagtgcgcgc acggcaacaa caagccaagg ccgcattcct tccccatgta 300
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ggatggagcg tgcaggtggg acaaacctta tttgacgctg ccaaatttgc acaataccgc 420
caaagcaggt tgcatacgca ggctgcagaa cagcgtttcg atgcggcacg cgaagaattg 480
ctgttgaaag ttgccgaaag ttatttcaac gttttactca gccgagacac cgttgccgcc 540
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aaaggtgctg ccaccgcgct ggatattcac gaagccaaag ccggttacga caatgccctg 660
gcccaagaaa tcgccgtatt ggctgagaaa caaacctatg aaaaccagt gaacgactac 720
accgacctgg atagcaaaca aatcgaggcc atagataccg ccaacctgtt ggcacgctat 780
ctgcccaagc tggaacgta cagtctggat gaatggcagc gcattgcctt atccaacaat 840
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aaccggctgg aagtaatacg ggcgcggcag gaagtcgcc aagcagaaca gaaactggct 1320
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 ttggaaacgg tatttgcgga ataa 1404

<210> 90

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 90

Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
 1 5 10 15

Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
 115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
 130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
 145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
 165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
 180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
 195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
225 230 235 240

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
245 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
385 390 395 400

~~Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln~~
~~405 410 415~~

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460

Phe Ala Glu
465

<210> 91

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 91

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<210> 92

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 92

gcggccgaat tccaacaggg tcaatgaagt

30

<210> 93

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 93

ctgttggaat tcggccgctt gtagcaaaca ggct

34

<210> 94

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 94

tagtacggtta ccgattcact tggtgctt

28

<210> 95
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 95
gcttggtgta ccatatgagc aaacaggctg aaaccagt 38

<210> 96
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 96
tcaatcctcg agttgcggct ttttctgctc tt 32

<210> 97
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 97
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<210> 98
<211> 33
<212> DNA
~~<213> Artificial Sequence~~

<220>
<223> Description of Artificial Sequence: primer

<400> 98
tatccaccaa ctggtcaatc gtggtcatatc cgg 33

<210> 99
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 99

ccacgctgat tattgcttcc ttccctgttg ctg

33

<210> 100

<211> 33

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<210> 101

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<210> 102

<211> 20

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<210> 103

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 103
gcctgacact gacgccctat ttgcaacatg aac 33

<210> 104
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 104
taccgtgctt gagccagttt ctgttctgct tgg 33

<210> 105
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 105
accgtgaggc ggacttggc 19

<210> 106
<211> 33
<212> DNA
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<223> Description of Artificial Sequence: primer

<400> 106
tggcccgcat tgcgggttt aaagccgtct tcg 33

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<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 108
<211> 20
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<223> Description of Artificial Sequence: primer

<400> 108
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<210> 109
<211> 20
<212> DNA
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<223> Description of Artificial Sequence: primer

<400> 109
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<210> 110
<211> 20
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<220>

<223> Description of Artificial Sequence: primer

<400> 110
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<210> 111
<211> 21
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 111
aagaccgtaa aaatgcaggc g 21

<210> 112
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 112

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20

<210> 113 .

<211> 20

<212> DNA

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<210> 114

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 114

attaaatatt ttgtccgctt gtac

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<210> 115

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 115

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33

<210> 116

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

13-07-1999

EP99401764.8

SEQL

<400> 116

agtgtcttta gcttcaatta cagcagcact gcc

33

115

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